



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6 4 August 1998 (04.08.98) EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE [BE/BE]; Rijnvischestraat 120, B-9052 Zwijnaarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS		
<b>(57) Abstract</b> <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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### Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant  
5 molecular biology. In particular, the invention relates to improvements of crop  
productivity of useful plants. One of the major limitations of crop productivity is the  
effect of environmental stress conditions on plant growth and development. An  
important goal of molecular biology is the identification and isolation of genes that can  
provide resistance or tolerance to such stresses. For agriculture, the creation of  
10 transgenic plants containing such genes provides the potential for improving the stress  
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on  
the growth of plants and the productivity of crops. The physiological response to these  
stresses arises out of changes in cellular gene expression. Expression of a number of  
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;  
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be  
classified into two groups: those that directly protect against environmental stresses  
and those that regulate gene expression and signal transduction in the stress  
response. The first group includes proteins that likely function by protecting cells from  
20 dehydration, such as the enzymes required for biosynthesis of various  
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,  
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,  
Bray et al., 1997). The second group of gene products includes transcription factors,  
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et  
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is  
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms  
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the  
30 hypothesis that the genetic information for tolerance to environmental stress conditions  
exists in all higher plants. In glycophytes, this information would only be expressed in  
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:  
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of  
35 evidence also demonstrate that even mild environmental stress conditions throughout  
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but



in particular yeast, especially *Saccharomyces*, is relatively easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by an non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO<sub>2</sub> etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

5 "Dehydration stress" is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole plant.

"Drought stress" refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

"Oxidative stress" refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms "salinity-induced stress", "salt-stress" or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

15 Said salt can be for example, water soluble inorganic salts such as sodium sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

20 The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

25 The terms "tolerance" and "resistance" cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability, 30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

35 The terms "tolerance" and "resistance" may be used interchangeably in the present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 $\mu$  plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5       The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10       The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15       The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20       (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25       (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30       Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T<sub>m</sub>) for the specific sequence at a defined ionic strength and pH. The T<sub>m</sub> is the temperature (under defined ionic strength and pH) at which  
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent  
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1  
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or  
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having  
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,  
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DFB2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (e) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (c) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

5  
10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more  
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

25 According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

30 More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;



(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not  
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the  
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence  
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means  
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of  
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and  
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5       The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10       The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous  
15       expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell  
20       enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any  
25       of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount  
30       effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably  
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method  
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a  
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a  
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a  
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,  
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said  
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced  
5 tolerance or resistance to environmental stress, said method comprising indirectly  
increasing or inducing the expression of an endogenous gene in said plant comprised  
within a polynucleic acid as defined above or indirectly increasing or inducing the activity  
of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

10 (a) introducing into the genome of a plant cell one or more recombinant DNA  
molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in  
said plant cell at an effective amount indirectly  
15 increases or induces the expression of an  
endogenous polynucleic acid or indirectly increases  
or induces the protein activity of a protein encoded by  
said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in  
the same transcriptional unit and under the control of  
20 said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence"  
meaning that said recombinant DNA molecule will comprise a sequence originating  
from a foreign species, or, if from the same species, may be substantially modified  
25 from its original form. For example, a promoter operably linked to a structural gene  
which is from a species different from which the structural gene was derived, or, if  
from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing  
a plant with enhanced tolerance or resistance to environmental stress conditions, said  
30 method comprising indirectly increasing or inducing the expression of an endogenous  
gene in said plant comprised within a polynucleic acid as defined above or indirectly  
increasing or inducing the activity of a protein of the invention as defined above.  
According to this embodiment, other polynucleic acids modulating the expression or  
the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of  
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,  
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of  
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and  
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example  
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The  
35 introduced sequence generally will be substantially identical to the endogenous



sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with  
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of  
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose  
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the  
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control  
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard  
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in  
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,  
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter  
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,  
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the  
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a  
5 constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein  
10 that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

15 According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

20 The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance  
25 to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined  
30 with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

35 The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative  
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a  
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can  
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,  
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various  
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress  
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of  
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardia glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.



The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5       The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10       The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein  
15       having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20       The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present  
25       invention also relates to the coding region as well as the promoter region of any of said genomic clones.

      The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30       The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the  
35       primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references  
5 mentioned herein are incorporated by reference.

## BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut fur Zuchtungsforschung, Koln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H<sub>2</sub>O<sub>2</sub> (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H<sub>2</sub>O<sub>2</sub> (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Zuchtungsforschung, Köln, Germany).

5                   Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to  
10                   OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

                  Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during  
15                   plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown  
20                   in b and d using a PhosphorImager (Molecular Dynamics).

                  Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
25                   section) upon applying a salt stress of 200 mM NaCl overnight.

                  Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left  
30                   section) upon applying an osmotic stress induced by 20% PEG overnight.

                  Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H<sub>2</sub>O<sub>2</sub>, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H<sub>2</sub>O<sub>2</sub> (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.



## **EXAMPLES**

### **Example 1. Construction of the cDNA library.**

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H<sub>2</sub>O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)<sub>14</sub>-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

### **Example 2. Yeast transformation and selection for osmotolerance.**

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD<sub>600</sub> at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

### Example 3. Characterization of *At-DBF2*.

*At-DBF2*, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

### Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive  
5 role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

**Example 5. Both *At-DBF2* and *DBF2* can functionally complement the  
10 *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-DBF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the  
15 overexpression of both *DBF2* and *At-DBF2* (Figure 4).

**Example 6. *At-DBF2* is cell cycle regulated.**

*DBF2* expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4  
20 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul  
*et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S  
25 phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases  
30 until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

**Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction**

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

**Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells**

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

**Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress**

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif<sup>R</sup> (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

**Example 10. Tolerance to environmental stress in plant cells**

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of the three lines at least five times higher than the fresh weight of the control transgenic calli.

**Example 11. Tolerance to environmental stress in plants.**

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefore seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l<sup>-1</sup> sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated



twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

#### Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 gm<sup>-3</sup> denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

**Tabel 1**

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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**TABLE 2**  
**EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF**  
**THE PRESENT INVENTION**

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
$\alpha$ -amylase ( <i>Amy32b</i> )	Aleurone	Lanahan <i>et al</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin $\beta$ -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AiPRP4	Flowers	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
chalcone synthase ( <i>chsA</i> )	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; <a href="http://winetitles.com.au/gwrdc/csh95-1.html">http://winetitles.com.au/gwrdc/csh95-1.html</a>
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AiPRP4	Leaf	<a href="http://salus.medium.edu/mmg/tierney/html">http://salus.medium.edu/mmg/tierney/html</a>
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
$\beta$ -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	<a href="http://salus.medium.edu/mm/tierney/html">http://salus.medium.edu/mm/tierney/html</a>
RD2 gene	root cortex	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
TobRB7 gene	root vasculature	<a href="http://www2.cnsu.edu/ncsu/research">http://www2.cnsu.edu/ncsu/research</a>
AtPRP4	leaves; flowers; lateral root primordia	<a href="http://salus.medium.edu/mm/tierney/html">http://salus.medium.edu/mm/tierney/html</a>
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws118	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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**Claims**

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
  - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
  - (a) SEQ ID NO 1, or the complementary strands thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

- 10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of
- 20 (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 25 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

- 35 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- 5
- (a) SEQ ID NO 5, or the complementary strand thereof;
  - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
  - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
  - 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined  
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of  
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,  
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,  
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or  
120.

13. A method for producing a plant with enhanced tolerance or resistance to  
environmental stress, said method comprising transiently introducing into a plant  
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of  
claims 2 to 10 which is expressed in an amount effective to confer enhanced  
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to  
30 environmental stress, said method comprising stably introducing into a plant cell a  
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2  
to 10 which is expressed in an amount effective to confer enhanced tolerance or  
resistance to environmental stress.

35

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5
16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10
17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
- 15
18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
  - a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 20
19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,
- 25
- 30



- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:  
a polynucleic acid according to or as defined in any of claims 2 to 10, and,  
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:  
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,  
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 25 23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
- 30 24. The recombinant polynucleic acid of claim 21 comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 30 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
- 35 36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

5

```
At-DBF2    DAGYFDDFWHEADIAKYADVFNQQCRALTAVDSSVSKLVGFTFRHRNGKQGSGMLFNGLHSDPESTFY  528  
          /-----/ .-----/ :-----/ |-----/ ||-----/ |-----/ ||-----/ |  
          /-----/ .-----/ :-----/ |-----/ ||-----/ |-----/ ||-----/ |  
          /-----/ .-----/ :-----/ |-----/ ||-----/ |-----/ ||-----/ |  
  
      DBF2    DAGYFDDFTSEADMAYADVFVKRQDKLTAMVDSSVSKLVGFTFRHRNGKQGSGILFNGLHSDPESTFY  572
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**FIGURE 1 A**

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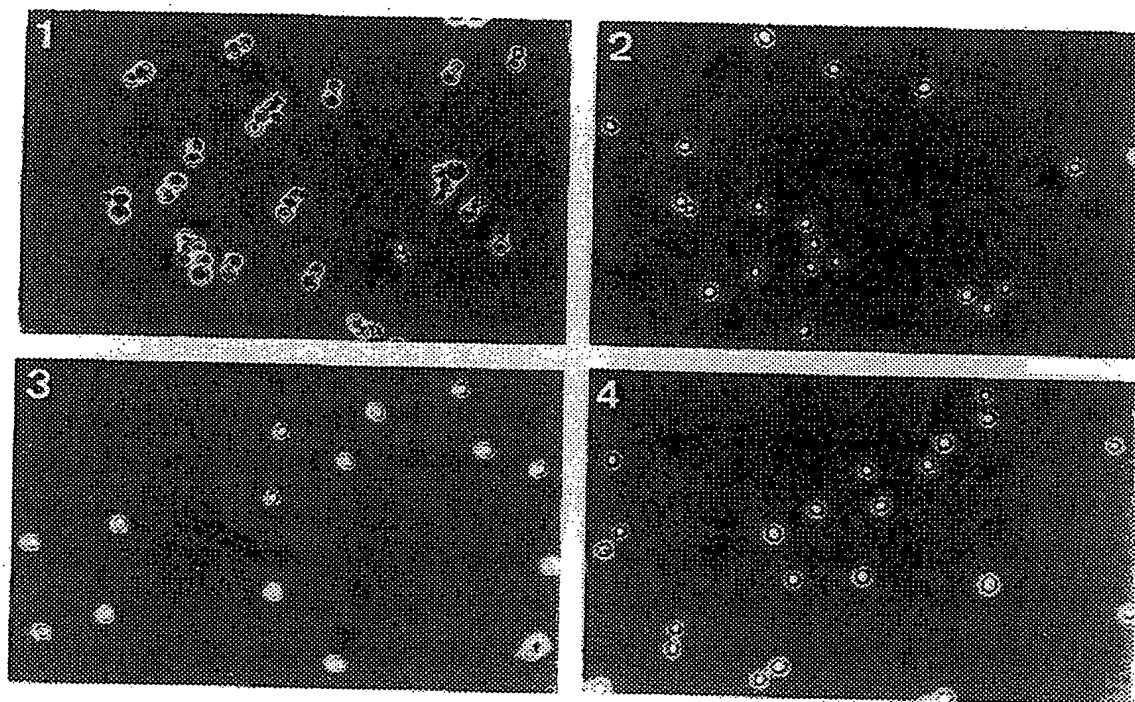


FIGURE 1B

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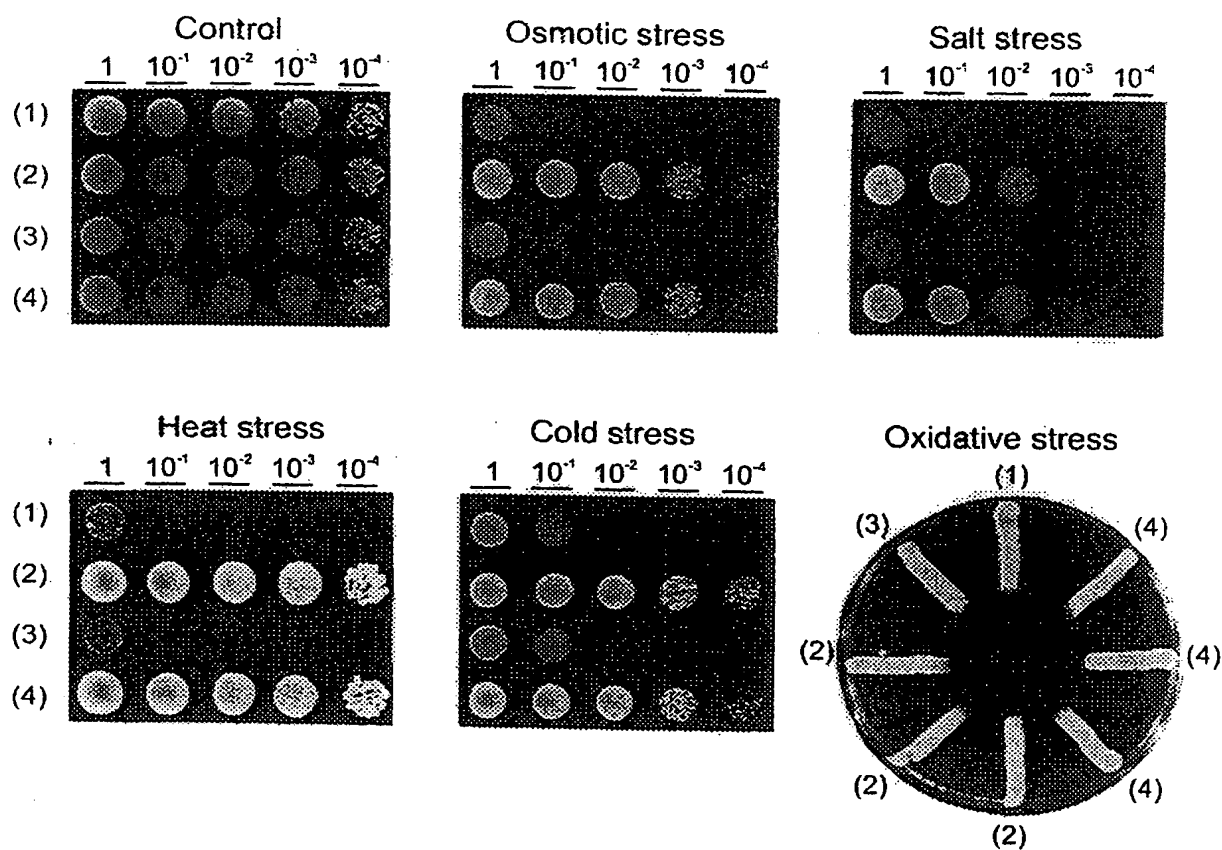


FIGURE 2

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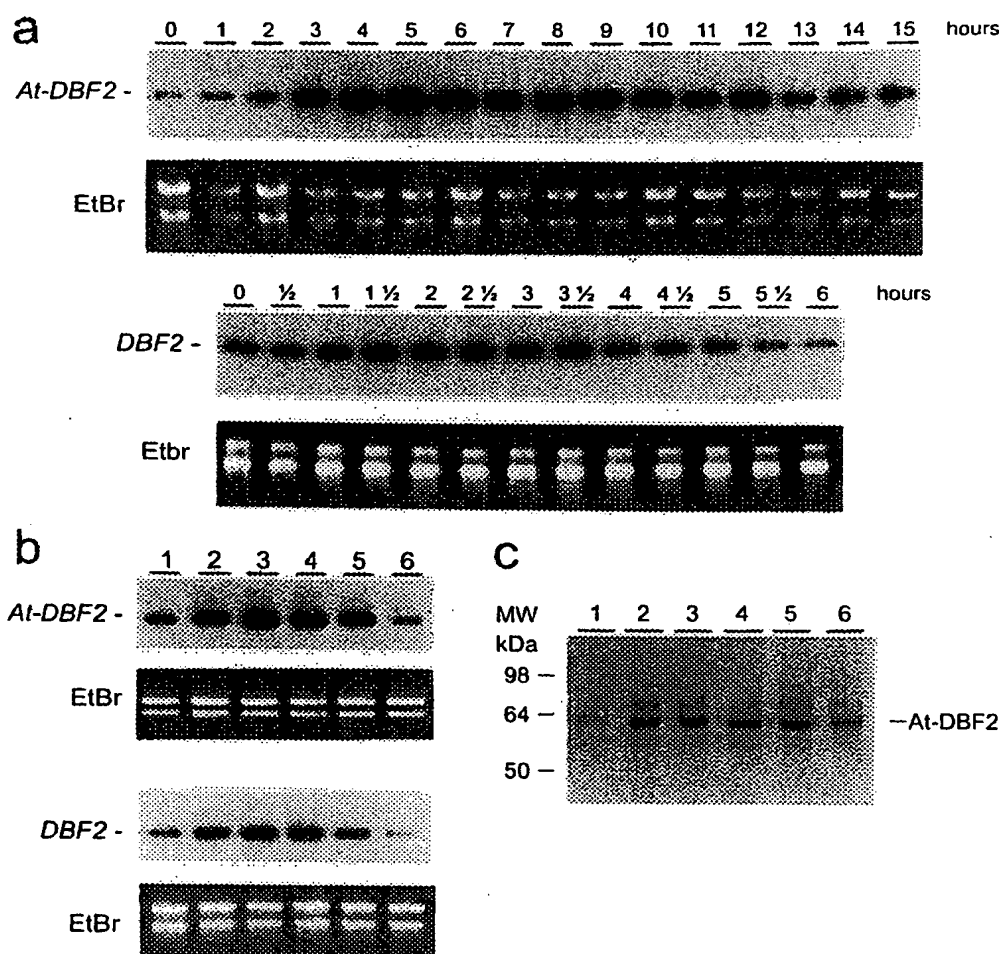


FIGURE 3

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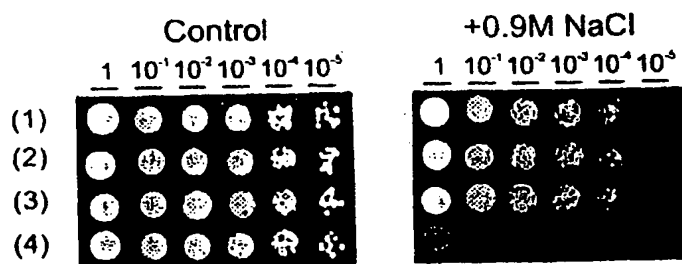


FIGURE 4

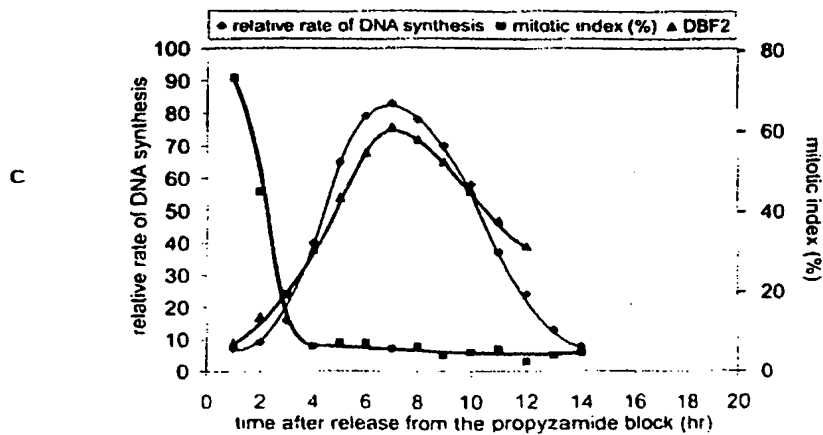
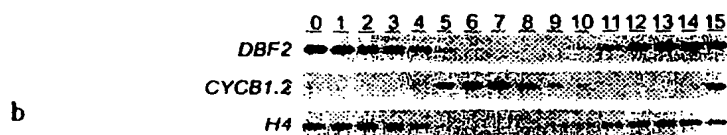
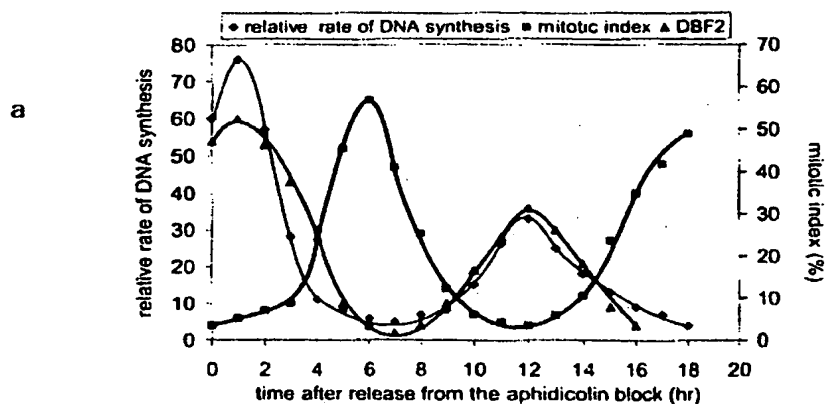


FIGURE 5



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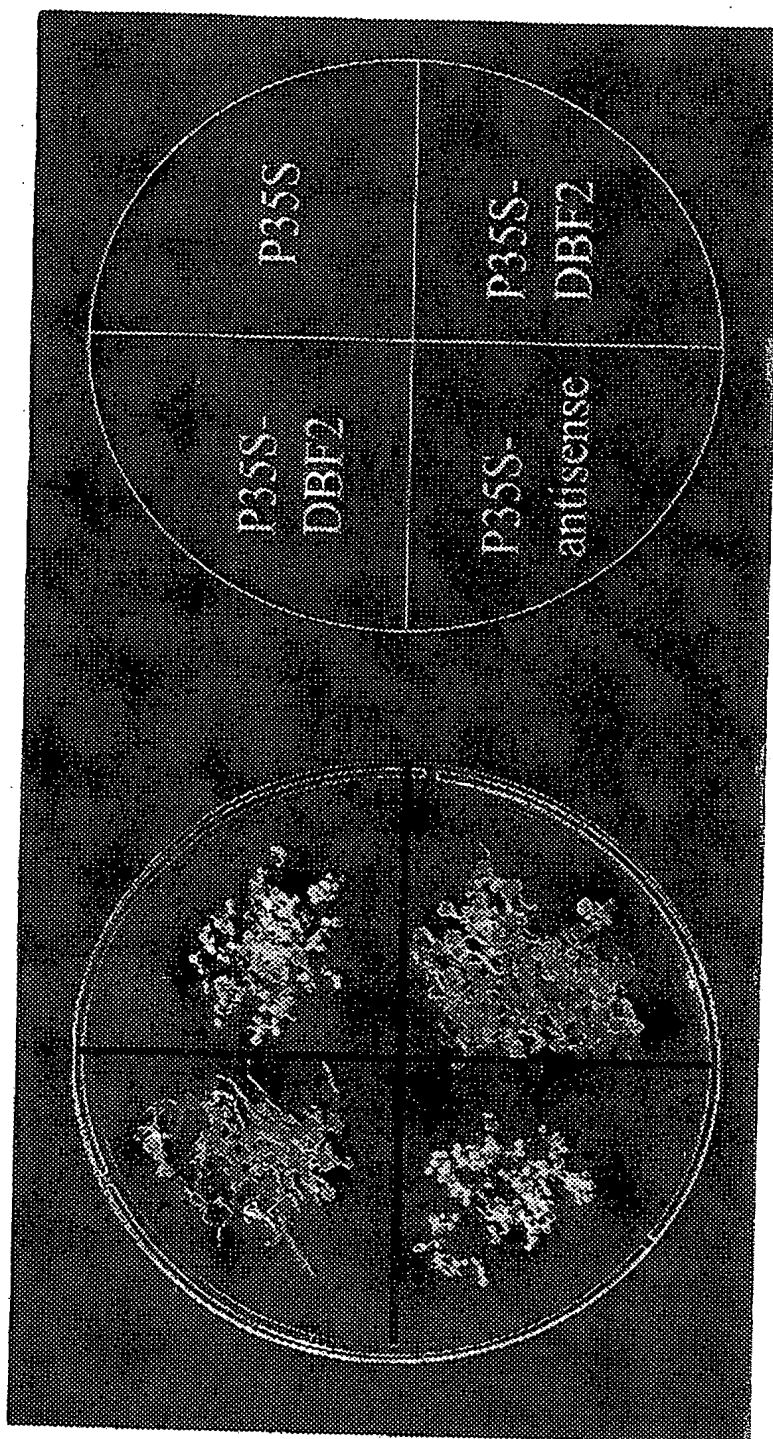


FIGURE 6

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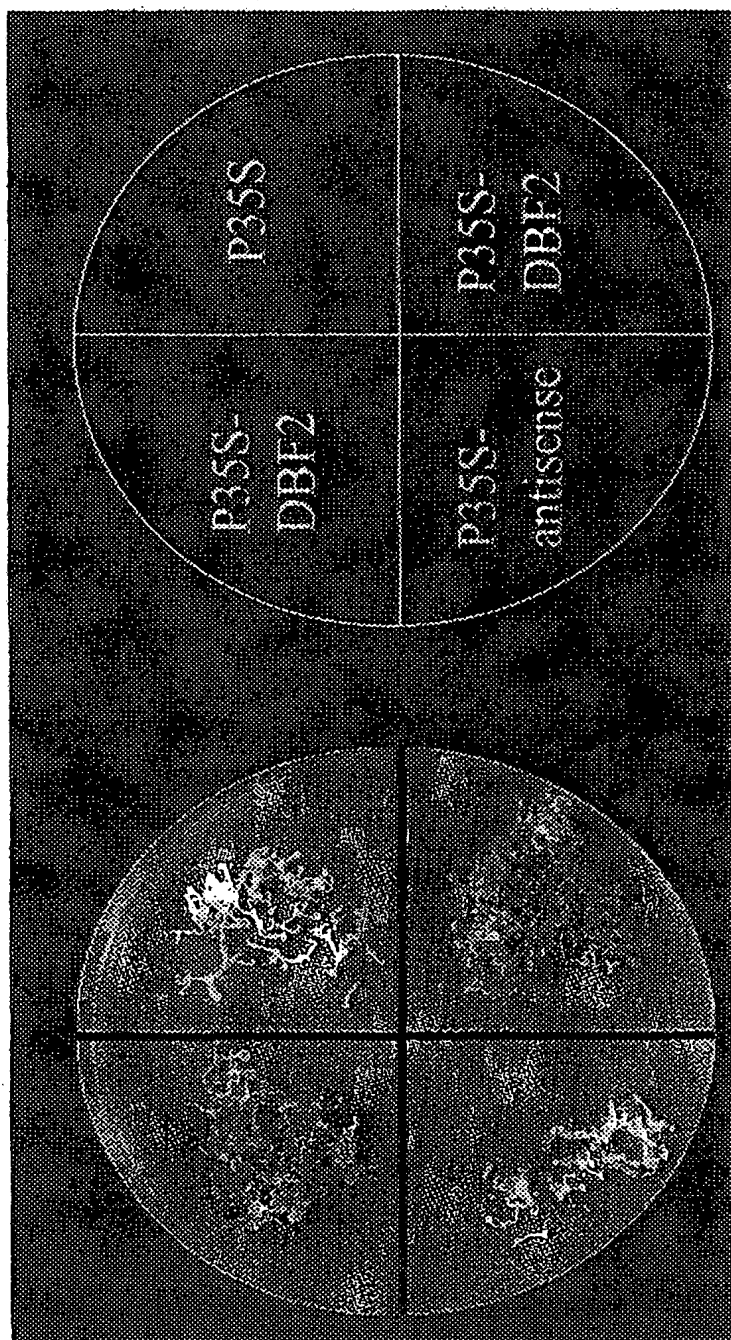


FIGURE 7

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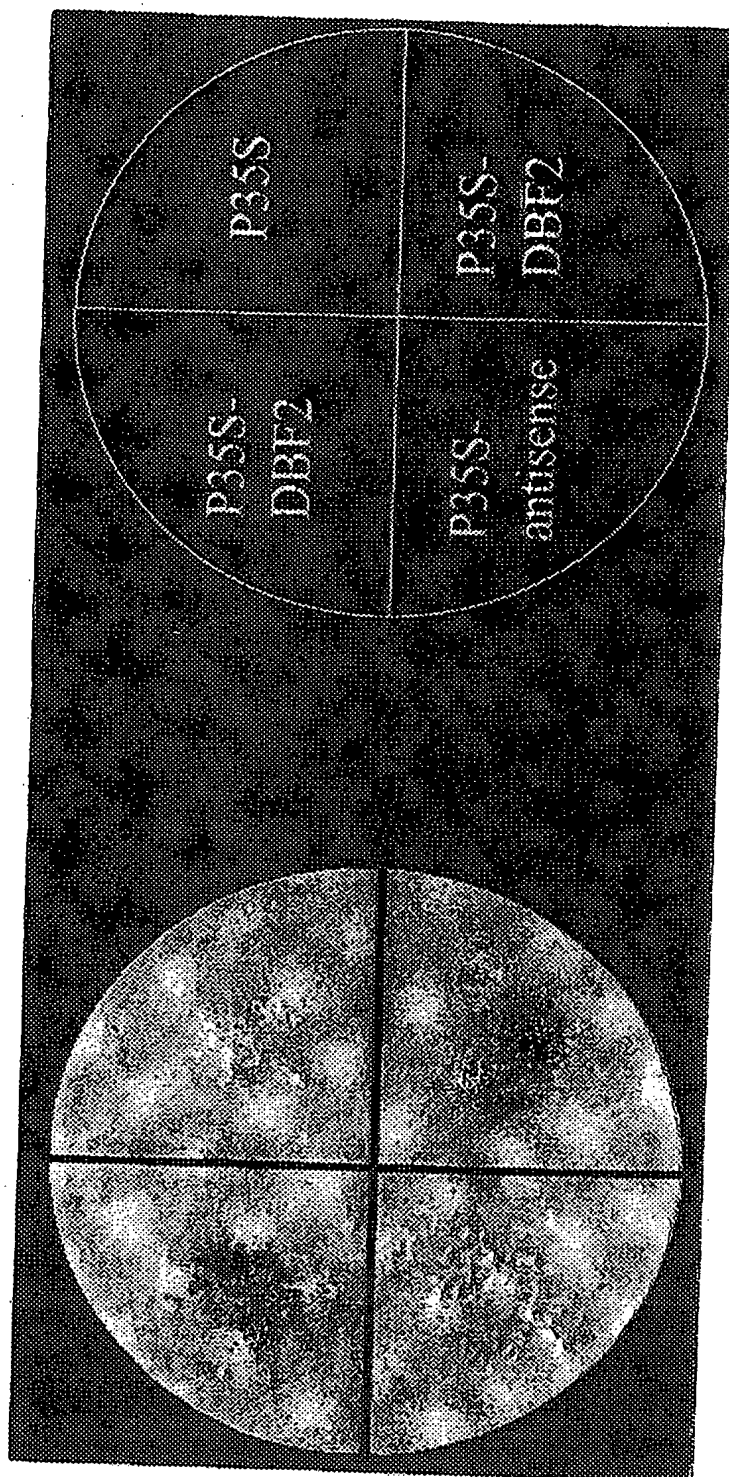


FIGURE 8

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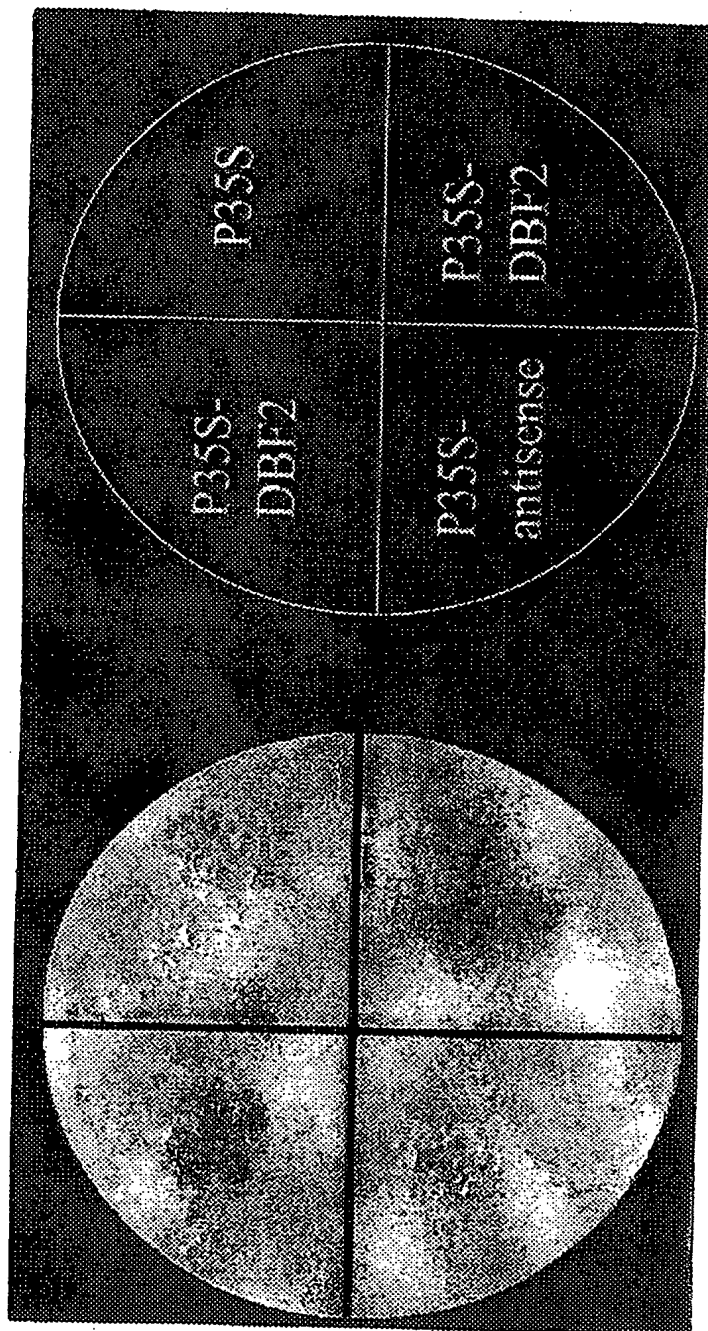


FIGURE 9

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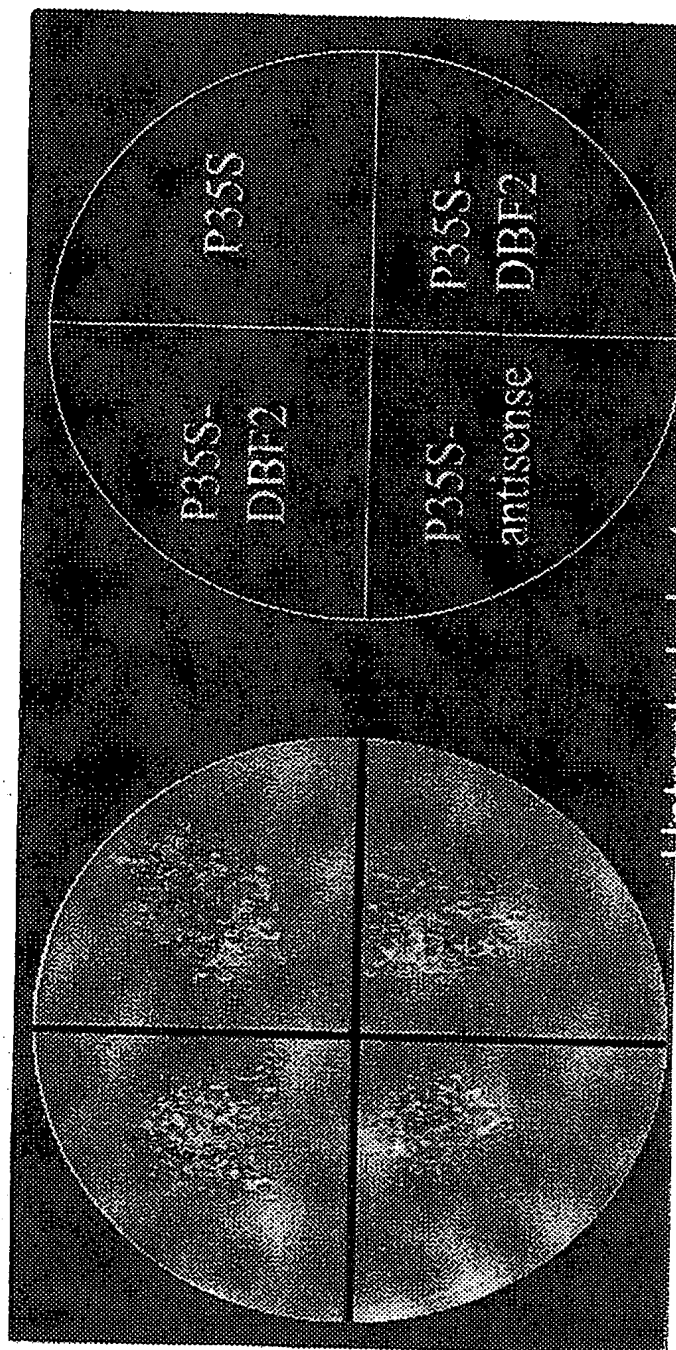


FIGURE 10

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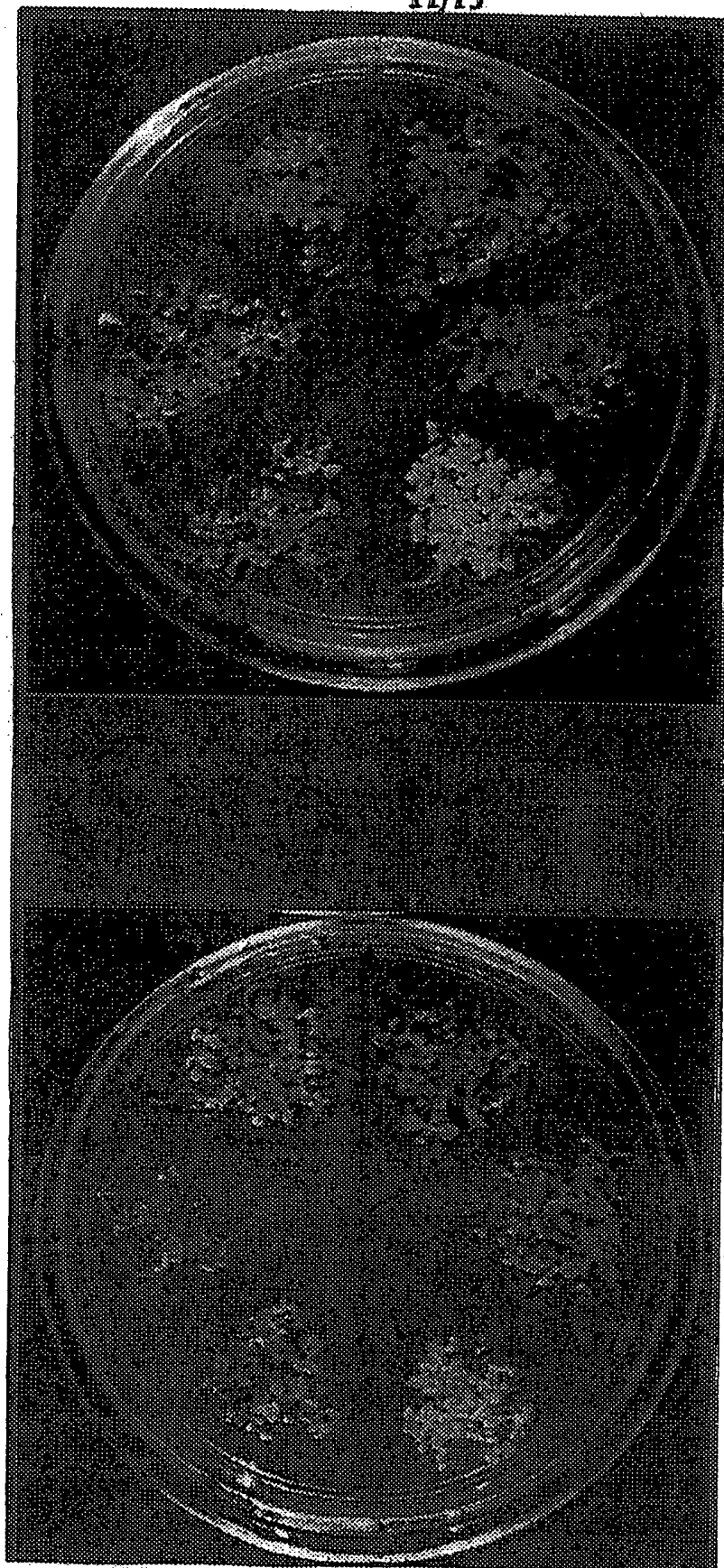


FIGURE 11

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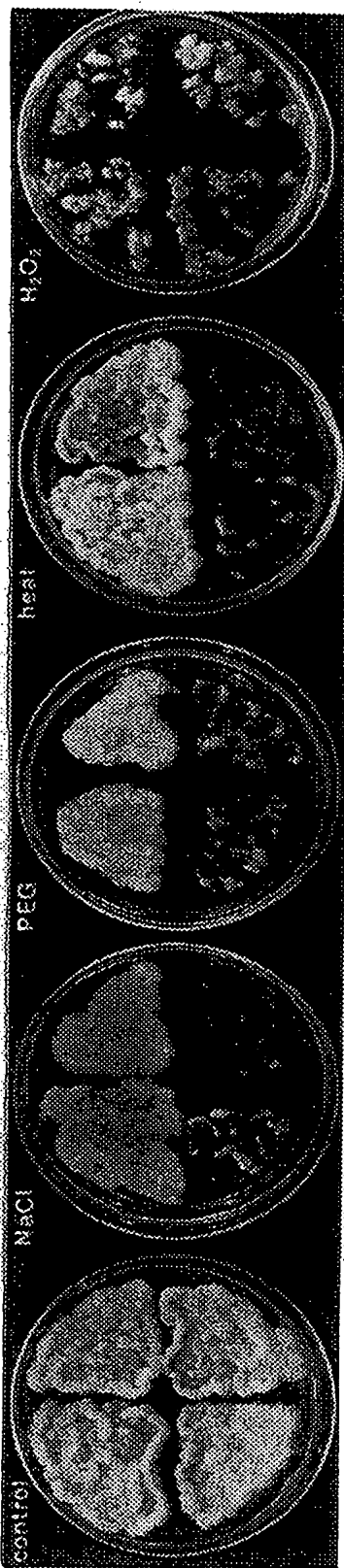


FIGURE 12A

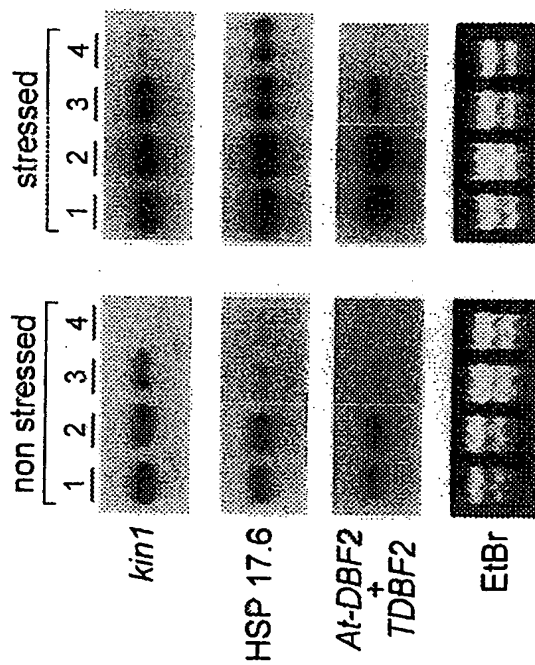


FIGURE 12c

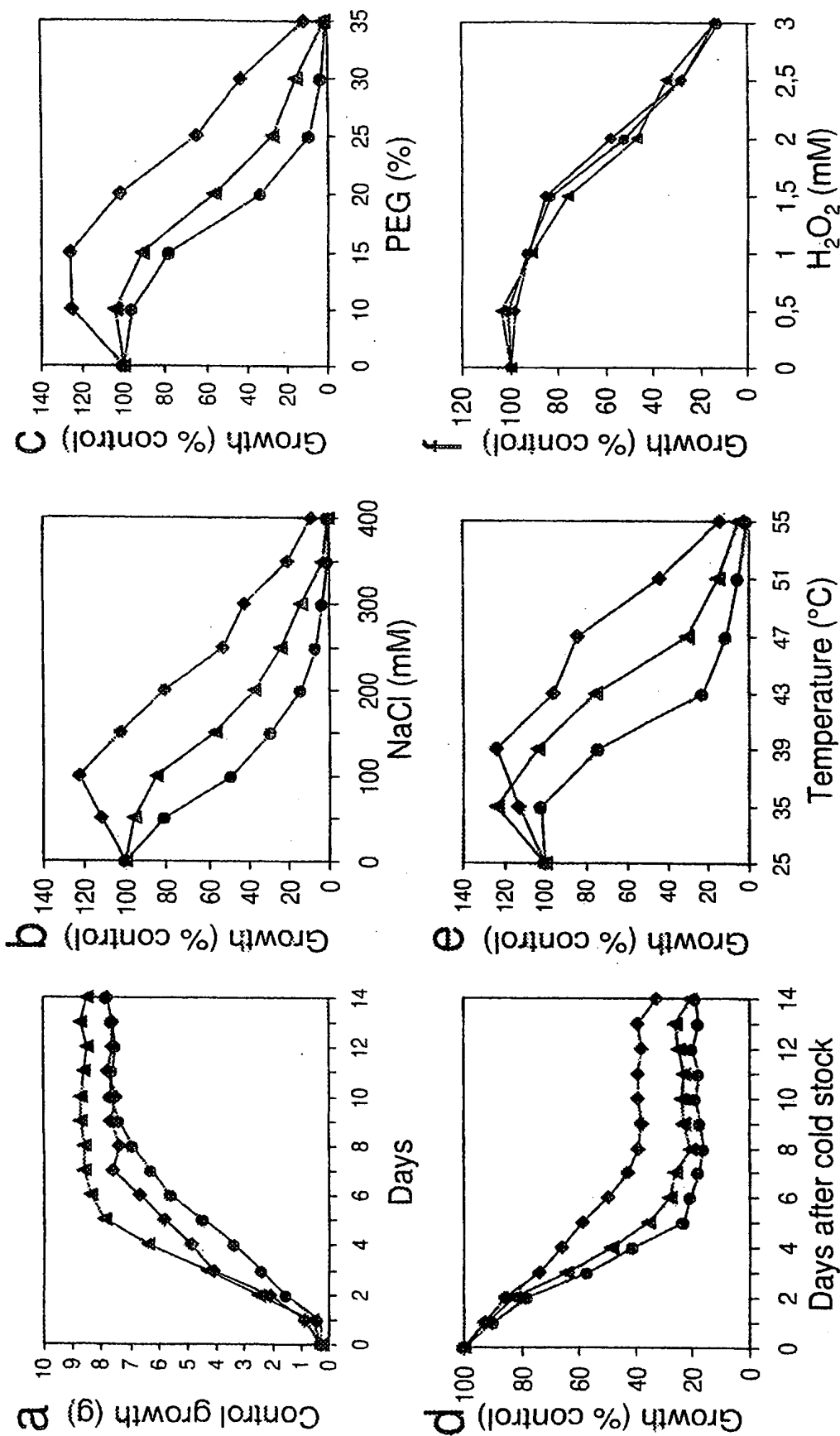


FIGURE 12B





FIGURE 13

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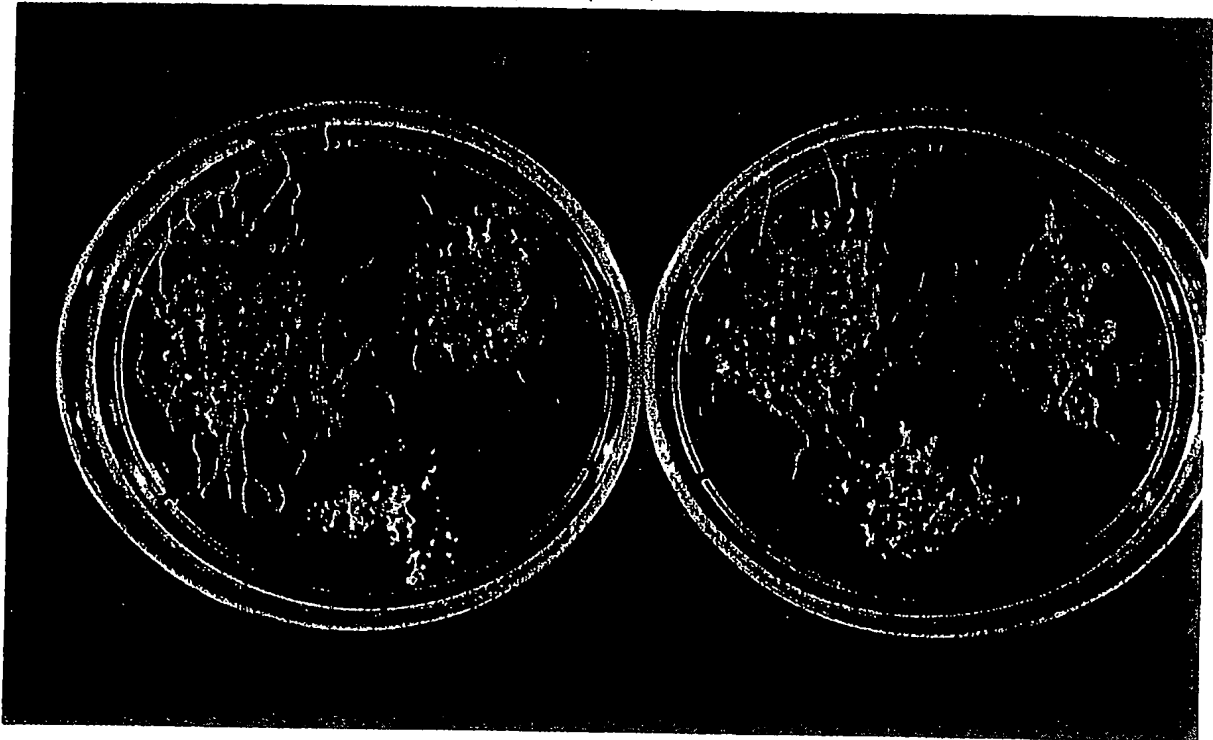


FIGURE 14

## SEQUENCE LISTING

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<140>

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<151> 1998-08-04

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                                         1          5

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              10              15              20

ttc ccc aat cag aac cta acg aaa aga aga acg cgt cca gcg ggt atc      150
Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
              25              30              35

aac gac tcg cct tcg ccg gtg aaa tgc ttt ttt ttc ccc tat gaa gac      198
Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe Phe Pro Tyr Glu Asp
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              55              60              65

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Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
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tct gac cag atc aag ctc aac gaa gag tgg tcc tcc tat tta cag aga	486
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gagctcgcca	gcctgcccag	cctttcgccc	cagcctgcca	gccttttttt	aaacgctgaa												1816			
aaacgcctaa	aaaaatcgaa	ctttaaacgc	ttttaaaacg	gctgcccata	aaaaaaaaag												1876			

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1909

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<211> 528

<212> PRT

<213> Arabidopsis thaliana

<400> 2

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      20           25           30
Arg Pro Ala Gly Ile Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe
      35           40           45
Phe Pro Tyr Glu Asp Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln
      50           55           60
Pro Thr Lys Tyr Ser Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe
      65           70           75           80
Tyr Glu Arg Ala Thr Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg
      85           90           95
Ala Met Tyr Phe Leu Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile
      100          105          110
Ser Arg Arg Gln Arg Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln
      115          120          125
Ser Gln Leu Pro Asn Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser
      130          135          140
Ser Tyr Leu Gln Arg Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys
      145          150          155          160
Pro Lys Asn Arg Asp Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly
      165          170          175
Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys
      180          185          190
Ala Leu Lys Ile Leu Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr
      195          200          205
Cys His Val Leu Thr Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu
      210          215          220
Thr Met Val Lys Leu Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly
      225          230          235          240
Met Ala Ile Glu Ser Glu Leu Gly Gly Asp Phe Arg Thr Glu Ser Ile
      245          250          255

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Gly Arg Arg Cys Leu Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu  
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 Met Phe Cys Ala Val Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser  
 275 280 285  
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 290 295 300  
 Phe Lys Asp Leu Gly Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp  
 305 310 315 320  
 Arg Arg Lys Leu Tyr Thr Cys Pro Asn Ser Met Val Gly Ser Pro Asp  
 325 330 335  
 Tyr Ile Ala Leu Glu Val Leu Arg Gly Lys Arg Tyr Glu Tyr Thr Val  
 340 345 350  
 Asp Tyr Trp Ser Leu Gly Cys Met Leu Phe Glu Ser Leu Val Gly Tyr  
 355 360 365  
 Thr Pro Phe Ser Gly Ser Ser Thr Asn Glu Thr Tyr Ala Ile Ser Arg  
 370 375 380  
 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala  
 385 390 395 400  
 Ala Phe Tyr Asn Arg Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp  
 405 410 415  
 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr  
 420 425 430  
 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe  
 435 440 445  
 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe  
 450 455 460  
 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln  
 465 470 475 480  
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu  
 485 490 495  
 Val Gly Phe Thr Phe Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly  
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&lt;210&gt; 3

&lt;211&gt; 695

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (94)..(564)

&lt;400&gt; 3

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gcacgagcaa gaaagttaac acaacagcta aga atg gat ttg gag ttt gga agg 114  
Met Asp Leu Glu Phe Gly Arg  
1 5

ttt cca ata ttt tca atc ctc gaa gac atg ctt gaa gcc cct gaa gaa 162  
Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu  
10 15 20

caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210  
Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp  
25 30 35

gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258  
Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp  
40 45 50 55

gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306  
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile  
60 65 70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354  
Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg  
75 80 85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402  
Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu  
90 95 100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450  
Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala  
105 110 115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498  
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val  
120 125 130 135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546  
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile  
140 145 150

caa gtt caa gtc gct tga gtttgtttgt gatccgtggt tttgtgtttt 594  
Gln Val Gln Val Ala  
155

aatgaatgta atcgataagc aactacctct tggtgttcgt tgtaaaatga aataaaaata 654

gttttctctg ttcataaaaa aaaaaaaaaa aaaactcgag c 695



&lt;210&gt; 4

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 4

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Met Leu Glu Ala Pro Glu Glu Gln Thr Glu Lys Thr Arg Asn Asn Pro
           20           25           30
Ser Arg Ala Tyr Met Arg Asp Ala Lys Ala Met Ala Ala Thr Pro Ala
           35           40           45
Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
           50           55           60
Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
           65           70           75           80
Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
           85           90           95
Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
           100          105          110
Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
           115          120          125
Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu
           130          135          140
Pro Lys Lys Pro Lys Thr Ile Gln Val Gln Val Ala
           145          150          155

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&lt;210&gt; 5

&lt;211&gt; 1311

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (133)..(1083)

&lt;400&gt; 5

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ttgccatttc tcagattccg gggaaagaaa aaaaaaacct agaaaagtgt tttctccggt 120
ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171
      Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
           1           5           10

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ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat 219  
 Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr  
 15 20 25

aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt 267  
 Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu  
 30 35 40 45

cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat 315  
 Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn  
 50 55 60

cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat 363  
 Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp  
 65 70 75

cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc 411  
 Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg  
 80 85 90

cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt 459  
 Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe  
 95 100 105

ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga 507  
 Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg  
 110 115 120 125

gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc 555  
 Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala  
 130 135 140

gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga 603  
 Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg  
 145 150 155

gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac 651  
 Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn  
 160 165 170

ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa 699  
 Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys  
 175 180 185

tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg 747  
 Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly  
 190 195 200 205

aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc 795  
 Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser  
 210 215 220

ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca 843  
 Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser  
 225 230 235

cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc 891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly  
 240 245 250

gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939  
 Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His  
 255 260 265

atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987  
 Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg  
 270 275 280 285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035  
 Glu Glu Glu Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser  
 290 295 300

tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga 1083  
 Ser Glu Tyr Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys  
 305 310 315

tactattttta cagaacaaaa gcatacatga gaagaaacgt ttaactaaag aattcagaag 1143

atttgattttt gataaaaaact tgtaccaatt tactgattaa gctttctggt gtcttagttt 1203

gtagctttttg gtttgtggaa aagtgttgta cacatcgta taacaccagg aacattaca 1263

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&lt;210&gt; 6

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 6

Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile Leu Val Arg  
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His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr Thr Thr Thr  
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 35 40 45

Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser  
 50 55 60

Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg  
 65 70 75 80

Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile  
 85 90 95

Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe  
 100 105 110

Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe  
 115 120 125

Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val  
 130 135 140  
 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp  
 145 150 155 160  
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile  
 165 170 175  
 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys  
 180 185 190  
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu  
 195 200 205  
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile  
 210 215 220  
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met  
 225 230 235 240  
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys  
 245 250 255  
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp  
 260 265 270  
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu  
 275 280 285  
 Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser Ser Glu Tyr  
 290 295 300  
 Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys  
 305 310 315

&lt;210&gt; 7

&lt;211&gt; 863

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (19)..(837)

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 gta gct ata ata acc gga gga gca aga ggg ata gga gcg gcc acg gcg 99  
 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala  
 15 20 25

aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt	147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
30 35 40	
gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt	195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
45 50 55	
cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta	243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
60 65 70 75	
gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg	291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag	531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac	627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga	771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Gly Phe Ile Thr Gly	
240 245 250	
cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg	819

His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met  
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aga ttt atc tac aac tag ttttcgtttg gtggtgtttc cttttc  
 Arg Phe Ile Tyr Asn  
 270

863

&lt;210&gt; 8

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 8

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Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu Asp Asn Glu Gly Ile  
 35 40 45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser  
 50 55 60

Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys  
 65 70 75 80

Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu  
 85 90 95

Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser  
 100 105 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala  
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser  
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys  
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser  
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp  
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn  
 195 200 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr  
 210 215 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

225		230		235		240
Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly His Asn Leu Val Val						
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 atatatgctc gtttttctaaa ctatttttta attggattga tgttcttaaa tcttaagggt 174  
 caaaatactt tttatgctca aaaacttact taaattctgt gatcgcttga acctaagtgg 234  
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 attaagtaat catcaacaaa atgattgatc agatctatca atacaagtgt attttttttt 534  
 cacatacaaaa aaaattatct caccgacgaa aaaaaataa aaaattatta tgtagatcca 594  
 tcgaacaaaa ggcttgaata tcggaagtca cttaaaagt taataatcga ataaatatta 654  
 gtggataaaa tgaaatttat ctacaaccct actctccgac atgttactgt ttgcgtcatc 714  
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 ccggatccga tcaggaaaacg ggttttgata tgtttcgggt tacgacaaaa aattagggct 834  
 ttttatcaaa tcaatcagtt ggtagtaaaa ttttgtggat tgttcttgtc gattccgttt 894  
 gattgttgac caaatttctt cctaggattt tgttgataat cgatcgtata atggtgattg 954  
 cag tat cgt cct tca agc gcg tac aac gcc cca ttc tac acc aca aac 1002  
 Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn  
 10 15 20  
 ggt ggt gct cca gtc tcc aac aac atc tct tcc ctc acc atc gga gaa 1050  
 Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser Leu Thr Ile Gly Glu  
 25 30 35  
 aga g gtatcgtaac cctgaatttc aagagtctat caataagaat cggaacttgt 1104  
 Arg G  
 tggatttatg aaagagataa aactgagata tagagtctaa gctgagatct gttcgtgaag 1164  
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 ly Pro Val Leu  
 40  
 ctt gag gat tat cat ttg atc gag aag gtt gct aat ttc acc aga gag 1267  
 Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu  
 45 50 55  
 agg atc cct gag aga gtg gtt cat gct aga gga atc agt gct aag ggt 1315  
 Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly  
 60 65 70  
 ttc ttt gaa gtc acc cat gac att tca aac ctc act tgt gct gat ttt 1363  
 Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe  
 75 80 85  
 ctc aga gcc cct ggt gtt caa act ccg gtt att gtc cgt ttc tca acg 1411  
 Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val Arg Phe Ser Thr  
 90 95 100 105  
 gtt gtt cac gga cgt gcc agt cct gaa acc atg agg gat att cgt ggt 1459  
 Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly  
 110 115 120



ttt gct gtc aag ttt tac acc aga gag gtataagaaa gattcaaagt 1506  
 Phe Ala Val Lys Phe Tyr Thr Arg Glu  
 125 130

ttccattttt aatcgtcttt tagcttcttt agaatcagga ctgatttttg tcttggtact 1566

gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616  
 Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe  
 135 140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664  
 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys  
 145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712  
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr  
 160 165 170 175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760  
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 180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808  
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val  
 195 200 205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856  
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys  
 210 215 220

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gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952  
 Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu  
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cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000  
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 260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048  
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu  
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ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144  
 Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr  
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gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192  
 Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
cag aga cat cgc ctt gga ccg aat tat ttg cag ctt cca gtc aat gct				2288
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc				2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca				2384
Met His Arg Asp Glu Glu	385			
ttgttagtct ttttacttgg aatcaaaaatt ctcatttggg ttgtactttt tacag atc				2442
			Ile	
			390	
aat tac tac ccc tca aag ttt gat cct gtc cgc tgc gct gag aaa gtt				2490
Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
ccc acc cct aca aac tcc tac act gga att cga aca aag gtccgattcc				2539
Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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agaaaacctt ttaattgcta atgttgcag tgc gtc atc aag aaa gag aac aac				2652
		Cys Val Ile Lys Lys Glu Asn Asn		
		420	425	
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Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln	430	435	440	
gac agg ttt gtt aag aga tgg gtg gag att cta tgc gag cca cgt ctc				2748
Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
acc cac gag atc cgc ggc atc tgg acc tct tac tgg ctc aag				2790
Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
gtcagaacca aaaaaacact cgggtcaaatt tctacgtcct ttttaccaag tttcagcaaa				2850
ctaaaacatt atttatctct ctgtatctct cag gct gat cga tcc ttg gga cag				2904
		Ala Asp Arg Ser Leu Gly Gln		
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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 Gln Thr Pro Val Ile Val Arg Phe Ser Thr Val Val His Gly Arg Ala  
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 Ser Pro Glu Thr Met Arg Asp Ile Arg Gly Phe Ala Val Lys Phe Tyr  
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 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys  
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 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr  
 165 170 175  
 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp  
 180 185 190  
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val  
 195 200 205  
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys  
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 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu

225	230	235	24
Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu	245	250	255
His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile	260	265	270
Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu	275	280	285
Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val	290	295	300
Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr	305	310	315
Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr	325	330	335
Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380
Met His Arg Asp Glu Glu Ile Asn Tyr Tyr Pro Ser Lys Phe Asp Pro	385	390	395
Val Arg Cys Ala Glu Lys Val Pro Thr Pro Thr Asn Ser Tyr Thr Gly	405	410	415
Ile Arg Thr Lys Cys Val Ile Lys Lys Glu Asn Asn Phe Lys Gln Ala	420	425	430
Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln Asp Arg Phe Val	435	440	445
Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu Thr His Glu Ile	450	455	460
Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys Ala Asp Arg Ser Leu Gly	465	470	475
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 caa gct gag att aac cag ctt ctt agc ttg atc atc aac acg ttc tac 156  
 Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr  
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 Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp  
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                           Ala Leu Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp  
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 Lys Ser Lys Leu Asp Gly Gln Pro Glu Leu Phe Ile Arg Leu Val Pro  
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 gac aag cct aat aag acg ctc tca att att gac agt ggt att ggc atg 652  
 Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met  
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Asp Leu Val Asn  
95

aac ttg gga acc att gcg agg tct gga aca aaa gag ttt atg gag gcg 804  
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100 105 110

ctt caa gct gga gct gat gta agc atg ata gga caa ttt ggt gtt ggt 852  
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115 120 125

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Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val Val Thr Thr Lys  
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cac aat gat gat gaa caa tac gtt tgg gag tct caa gct ggt ggt tcc 948  
His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly Ser  
150 155 160

ttc act gtc act agg gat gtg gat ggg gaa cca ctt ggt aga gga act 996  
Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly Thr  
165 170 175

aag atc agc ctc ttc ctt aag gac gat cag gtaaggaatc gtagctttga 1046  
Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln  
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catgcag ctt gaa tac ttg gag gag agg aga ctc aaa gac ttg gtg aag 1155  
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220 225 230

aaa gaa aac gaa ggt gag gtt gaa gaa gtt gat gag aag aag gag aaa 1299  
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Asp Gly Lys Lys Lys Lys Lys Ile Lys Glu Val Ser His Glu Trp Glu  
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Leu Ile Asn Lys Gln Lys Pro Ile Trp Leu Arg Lys Pro Glu Glu Ile  
270 275 280

act aag gaa gag tat gct gct ttc tac aag agc ttg acc aat gac tgg 1443  
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285 290 295

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 Glu Ile Leu Gly Asp Lys Val Glu Lys Val Val Val Ser Asp Arg Ile  
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 Thr Ser Gly Phe Ser Leu Asp Glu Pro Asn Thr Phe Ala Ala Arg Ile  
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 Glu Arg Arg Leu Lys Asp Leu Val Lys Lys His Ser Glu Phe Ile Ser  
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 Tyr Pro Ile Tyr Leu Trp Thr Glu Lys Thr Thr Glu Lys Glu Ile Ser  
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 His Phe Ser Val Glu Gly Gln Leu Glu Phe Lys Ala Ile Leu Phe Val  
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 95 100 105  
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gca ttc cga aca gat gag att aga aga aca cct cca acc cca caa gat Ala Phe Arg Thr Asp Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp 220 225 230 235			722
gaa atg aga gct gga atg agt tat ttc cac gag aca atc tgg aaa ggt Glu Met Arg Ala Gly Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly 240 245 250			770
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Thr Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr	
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Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile	
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Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr	
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Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
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Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
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Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
560 565 570	

cct gcc gct gtt gca aga ctc ttt tct ata gac tgg tac aaa aac cgt	1778
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Lys	Glu	Ile	Met	Gln	Ser	Ser	Lys	Ser	Ala	Gln	Glu	Leu	Val	Lys	Leu	
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Tyr	Asp	Ala	Leu	Leu	Leu	Asp	Arg	Phe	Leu	Asp	Ile	Leu	Gln	Asp	Leu
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Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser
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Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Pro Glu Ala
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tct aga ttc gtt aac aga cat ctc ttt cct tat atg cac a gtaagttata 294
Ser Arg Phe Val Asn Arg His Leu Phe Pro Tyr Met His L
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gattcgaatt ttgctatgaa gttttggtct ttgtgaacat gttcagggttt gtaaattgcc 474

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Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys Gly Met Val Lys Arg
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Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly Ser Cys Cys Leu
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Gln Arg His Gly Asn Pro Ile Pro Leu Arg Arg Pro Ala Met Thr Ala			
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Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu			
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46



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Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser Lys Glu Val Ser Arg Ser  
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 Gly Lys Lys Arg Pro Met Glu Ser Ser Thr Tyr Ser Leu Ile Asp Asp  
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 Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn Asp Thr Ser Gly His Glu  
                                  245                      250                      255  
 Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg  
                                  260                      265                      270  
 Arg Arg Lys Lys Ser Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu  
                                  275                      280                      285  
 Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly  
                                  290                      295                      300  
 Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr  
                                  305                      310                      315                      320  
 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln  
                                  325                      330                      e                      335  
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe  
                                  340e                      345                      350  
 Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly  
                                  355y                      360                      365  
 Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly  
                                  370                      375                      380  
 Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r  
                                  385                      390                      395u  
 Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu  
                                  400                      405                      410  
 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg  
                                  415                      420                      425  
 Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn  
                                  430                      435                      440  
 Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys

445                      450                      455                      460  
 Val Trp Lys Asn Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln Val  
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 Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe Phe  
                                  480                      485                      490  
 Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys Asp  
                                  495                      500                      505  
 Leu Gly Met Phe Asp Lys Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala  
                                  510                      515                      520  
 Leu Arg Ile Lys Ile Arg Asn Thr Leu Ile Glu Leu Phe Arg Val Ser  
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 Asp Gln Thr Glu

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 ggc act cgc ttg aga cca ttg act ctc agt ttc cca aag ccc ctt gtt 99  
 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val 25  
                                  15                      20  
 gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag 147  
 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys 40  
                                  30                      35  
 gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195  
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu 55  
                                  45                      50  
 gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243  
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys 70  
                                  60                      65  
 atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291  
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu 90  
                                  75                      80                      85  
 gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339  
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe

95										100										105											
gtt	ctt	aac	agt	gat	gtg	att	agt	gag	tac	cct	ctt	aaa	gaa	atg	ctt																
Val	Leu	Asn	Ser	Asp	Val	Ile	Ser	Glu	Tyr	Pro	Leu	Lys	Glu	Met	Leu															387	
			110					115					120																		
gag	ttt	cac	aaa	tct	cac	ggt	ggg	gaa	gcc	tcc	ata	atg	gta	aca	aag																
Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys															435	
			125				130					135																			
gtg	gat	gaa	ccg	tcg	aaa	tat	gga	gtg	gtt	gtt	atg	gaa	gaa	agc	act																
Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr															483	
			140				145				150																				
gga	aga	gtg	gag	aag	ttt	gtg	gaa	aag	cca	aaa	ctg	tat	gta	ggg	aac																
Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn															531	
					160					165					170																
aag	atc	aac	gct	ggg	att	tat	ctt	ctg	aac	cca	tct	gtt	ctt	gat	aag																
Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys															579	
				175					180					185																	
att	gag	cta	aga	ccg	act	tca	atc	gaa	aaa	gag	act	ttc	cct	aag	att																
Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile															627	
			190					195					200																		
gca	gca	gcg	caa	ggg	ctc	tat	gct	atg	gtg	cta	cca	ggg	ttt	tgg	atg																
Ala	Ala	Ala	Gln	Gly	Leu	Tyr	Ala	Met	Val	Leu	Pro	Gly	Phe	Trp	Met															675	
			205				210					215																			
gac	att	ggg	caa	ccc	cgt	gac	tac	ata	acg	ggg	ttg	aga	ctc	tac	tta																
Asp	Ile	Gly	Gln	Pro	Arg	Asp	Tyr	Ile	Thr	Gly	Leu	Arg	Leu	Tyr	Leu															723	
			220			225					230																				
gac	tcc	ctt	agg	aag	aaa	tct	cct	gcc	aaa	tta	acc	agt	ggg	cca	cac																
Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His															771	
			235			240				245				250																	
ata	gtt	ggg	aat	gtt	ctt	gtt	gac	gaa	acc	gct	aca	att	ggg	gaa	gga																
Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly															819	
				255				260					265																		
tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggg	cca	ggc	tgc	att	gtt	gag																
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu															867	
			270				275						280																		
tca	gga	gtc	aga	ctc	tcc	cga	tgc	acg	gtc	atg	cgt	gga	gtc	cgc	atc																
Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile															915	
			285				290					295																			
aag	aag	cat	gcg	tgt	atc	tcg	agc	agt	atc	atc	ggg	tgg	cac	tca	acg																
Lys	Lys	His	Ala	Cys	Ile	Ser	Ser	Ser	Ile	Ile	Gly	Trp	His	Ser	Thr															963	
			300			305					310																				
gtt	ggg	caa	tgg	gcc	agg	atc	gag	aac	atg	acg	atc	ctc	ggg	gag	gat																
Val	Gly	Gln	Trp	Ala	Arg	Ile	Glu	Asn	Met	Thr	Ile	Leu	Gly	Glu	Asp															1011	
			315			320				325					330																

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059  
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro  
                   335                                  340                                  345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107  
 His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met  
                   350                                  355                                  360

aa 1109

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                   20                                  25                                  30  
 Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu  
                   35                                  40                                  45  
 Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu  
                   50                                  55                                  60  
 Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu  
   65                                  70                                  75                                  80  
 Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys  
                   85                                  90                                  95  
 Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val  
                   100                                  105                                  110  
 Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His  
                   115                                  120                                  125  
 Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys  
                   130                                  135                                  140  
 Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe  
   145                                  150                                  155                                  160  
 Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile  
                   165                                  170                                  175  
 Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr  
                   180                                  185                                  190  
 Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu  
                   195                                  200                                  205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg  
 210 215 220  
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys  
 225 230 235 240  
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu  
 245 250 255  
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp  
 260 265 270  
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser  
 275 280 285  
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile  
 290 295 300  
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg  
 305 310 315 320  
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu  
 325 330 335  
 Ile Tyr Ser Asn Gly Gly Val Val Leu Pro His Lys Glu Ile Lys Ser  
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 Asn Ile Leu Lys Pro Glu Ile Val Met  
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 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98  
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe  
 15 20 25 30  
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146  
 Arg Ser Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly  
 35 40 45  
 aac gtg gct gtg gcg gct gct gct gct aca tcc act gag gcg cta aga aaa 194  
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys  
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914  
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala  
                   290                                  295                                  300

tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962  
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser  
                   305                                  310                                  315

att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010  
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys  
                   320                                  325                                  330

ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055  
 Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu  
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<213> Arabidopsis thaliana

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Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe Arg Ser  
                   20                                  25                                  30

Pro Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val  
                   35                                  40                                  45

Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile  
                   50                                  55                                  60

Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly  
                   65                                  70                                  75                                  80

Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu  
                   85                                  90                                  95

Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser  
                   100                                  105                                  110

Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys  
                   115                                  120                                  125

Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu  
                   130                                  135                                  140

Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val  
                   145                                  150                                  155                                  160

Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His  
                   165                                  170                                  175



Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp  
 180 185 190  
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro  
 195 200 205  
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly  
 210 215 220  
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly  
 225 230 235 240  
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys  
 245 250 255  
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn  
 260 265 270  
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser  
 275 280 285  
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr  
 290 295 300  
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys  
 305 310 315 320  
 Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val  
 325 330 335  
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 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95  
 Leu Glu Ile Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg  
 20 25 30  
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143  
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly  
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg	191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
50 55 60	
aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga	239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu His Arg	
65 70 75	
gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga	287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg	
80 85 90 95	
aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg	335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc	383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
115 120 125	
gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt	431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa	527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
160 165 170 175	
gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag	575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
180 185 190	
aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct	623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
195 200 205	
gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag	671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln	
210 215 220	
cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct	719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser	
225 230 235	
tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca	768
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala	
240 245 250	

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&lt;400&gt; 28

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 Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr  
 35 40 45  
 Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys  
 50 55 60  
 Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly  
 65 70 75 80  
 Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg  
 85 90 95  
 Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn  
 100 105 110  
 Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp  
 115 120 125  
 His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys  
 130 135 140  
 Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr  
 145 150 155 160  
 Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala  
 165 170 175  
 Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg  
 180 185 190  
 Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp  
 195 200 205  
 Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg  
 210 215 220  
 Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser  
 225 230 235 240  
 Ala Ala Ala Lys Pro Ser Val Thr Ala  
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&lt;211&gt; 1201

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

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ctctaagctt atcctcgttt tatgatctat tgatccttat tcaactcaaat gattctaata 115  
 ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167  
 Thr Glu Lys Ala Phe Leu Lys  
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217  
 Gln Pro Lys Val Phe Leu Se  
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277  
 tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325  
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly  
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373  
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu  
 35 40 45

gcc att gat g gtatgttttaa gcttttaact cgttataata gataaggaac 423  
 Ala Ile Asp G  
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 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly  
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 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala  
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 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu  
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 Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr  
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act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca 292  
 Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr  
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 Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala  
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gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att 388  
 Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile  
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Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met		
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Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met		
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Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp		
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cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc		1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe		
475	480	485
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga		1540
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495	500	505
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Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr		



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Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln		
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gta	aga	gag	agt	gat	tcg	ttg	aat	att	ttg	atg	gag	ttt	gtt	cct	ggt	484	
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cac	aac	aat	ggg	atc	atg	cat	cga	gat	att	aag	ggg	gca	aat	att	ttg	628	
His	Asn	Asn	Gly	Ile	Met	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu		
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Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys		
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Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly		
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Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala		
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Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	
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Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	395
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Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val	415	420	425	
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Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met	445	450	455	
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Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr	460	465	470	475
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Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser	480	485	490	
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Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala	525	530	535	

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 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg  
 275 280 285  
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys  
 290 295 300  
 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser  
 305 310 315 320  
 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu  
 325 330 335  
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile  
 340 345 350  
 Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg  
 355 360 365  
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu  
 370 375 380  
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly  
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp  
 405 410 415  
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr  
 420 425 430  
 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp  
 435 440 445  
 Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn  
 450 455 460  
 Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp  
 465 470 475 480  
 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp  
 485 490 495  
 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys  
 500 505 510  
 Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His  
 515 520 525  
 Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn  
 530 535 540  
 Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg  
 545 550 555 560  
 Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro  
 565 570 575  
 Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser  
 580 585 590  
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn  
 595 600 605  
 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu  
 610 615 620  
 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala  
 625 630 635 640  
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly  
 645 650

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<220>  
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&lt;400&gt; 35

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Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala	
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ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg	96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp	
20 25 30	
agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
50 55 60	
ccc cct cct cgt cag cct cca cgt cct cca aca gca ccg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
65 70 75 80	
atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg ccg agt aga	288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
85 90 95	
cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc			720
Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser			
225	230	235	240
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata			768
Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile			
	245	250	255
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc			816
Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr			
	260	265	270
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc			864
Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val			
	275	280	285
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa			912
Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu			
	290	295	300
ggg gga tgg ccg tat gcg gca ctc gag gag cat aag acg gag ccg gga			960
Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly			
305	310	315	320
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggc			1008
Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly			
	325	330	335
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggc gca			1056
Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala			
	340	345	350
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc			1104
Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile			
	355	360	365
aag ggc atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg			1152
Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala			
	370	375	380
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac			1200
Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn			
385	390	395	400
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga			1248
Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg			
	405	410	415
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg			1296
Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr			
	420	425	430
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg			1344
Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr			
	435	440	445

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
 450 455 460  
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
 465 470 475 480  
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
 485 490 495  
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
 500 505 510  
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
 515 520 525  
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635  
 Gly Arg Arg Trp Arg Glu  
 530 535  
 tggaccggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695  
 taaaaaaaaac caacaaaaaa aaaaaaaaaac aaaaaaaaaa a 1736

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 <211> 534  
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 <213> Arabidopsis thaliana

<400> 36  
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 Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro  
 35 40 45  
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala  
 50 55 60  
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala  
 65 70 75 80  
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg  
 85 90 95  
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp  
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln  
 115 120 125  
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met  
 130 135 140  
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg  
 145 150 155 160  
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala  
 165 170 175  
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val  
 180 185 190  
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn  
 195 200 205  
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly  
 210 215 220  
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser  
 225 230 235 240  
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile  
 245 250 255  
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr  
 260 265 270  
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val  
 275 280 285  
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu  
 290 295 300  
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly  
 305 310 315 320  
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly  
 325 330 335  
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala  
 340 345 350  
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile  
 355 360 365  
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala  
 370 375 380  
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn  
 385 390 395 400  
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg  
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr  
                   420                                  425                                  430  
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr  
                   435                                  440                                  445  
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met  
                   450                                  455                                  460  
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu  
                   465                                  470                                  475                                  480  
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr  
                                   485                                  490                                  495  
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro  
                                   500                                  505                                  510  
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr  
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 Gly Arg Arg Trp Arg Glu  
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 gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97  
 Ala Lys Lys Gly Ala Asn Leu Phe Lys  
                                   15                                  20  
 ccgctgaaaa ttctcagggc gcattctatc ccgcagaact ttcttgacca ctttgtag 155  
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203  
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys  
                                   25                                  30                                  35

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251  
 Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val  
                     40                    45                    50  
 gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299  
 Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp  
                     55                    60                    65  
 aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354  
 Lys Asp Asp Thr Leu  
                     70  
 ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406  
                                     Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile  
                                     75                                    80  
 ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454  
 Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg  
                     85                    90                    95                    100  
 aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503  
 Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys  
                     105                    110  
 accccc 508

<210> 38  
 <211> 112  
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                     20                    25                    30  
 Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys  
                     35                    40                    45  
 Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys  
                     50                    55                    60  
 Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro  
                     65                    70                    75                    80  
 Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys  
                     85                    90                    95  
 Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys  
                     100                    105                    110

<210> 39  
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 tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96  
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys  
 20 25 30  
 acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144  
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro  
 35 40 45

gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192  
 Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys  
 50 55 60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240  
 Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val  
 65 70 75 80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288  
 Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe  
 85 90 95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336  
 Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu  
 100 105 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384  
 Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr  
 115 120 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432  
 Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys  
 130 135 140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480  
 Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser  
 145 150 155 160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528  
 Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr  
 165 170 175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576  
 Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu  
 180 185 190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629  
 Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys  
 195 200

acttttagtat acattgaatt ggctttaag gtgtgtactt tgttgttttg ttacag gtg 688  
 Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736  
 Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser  
 205 210 215 220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784  
 Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys  
 225 230 235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832  
 Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser  
 240 245 250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881



His Cys Ile  
255

atgcagctta tctctgtttt aacttactag tgtggttggt tctttttgta g atc ata 938  
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986  
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala  
260 265 270

ggt tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034  
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys  
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090  
Met Gln  
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144  
Thr Ala Lys Ile Asn  
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192  
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly  
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240  
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln  
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtggt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355  
Asp Ser Phe Glu Asp  
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403  
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys  
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451  
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys  
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499  
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly  
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547  
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met  
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595  
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys  
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Lys Glu	
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ctctctcgag gactcatcat tattctctta accgcaactt ctttaccttc caaacactccc 6164  
ctgtacactt tagaattccc tccgtatccg atcatgttct catcggaaaa cccttttgtt 6224  
gcttccaaaa catctttgta ttgcactctg tgaggccaat actctgtttc ccaatcttcc 6284  
acgtctcctt ctagtctctg ccttcgacgc cttacaacgt agaaacagag gagcccaata 6344  
acagagacta acaacacaac accactagag accccagcaa tgaagccttt agacttcaaa 6404  
acagagtcac ctgacaattt aaacgaaggt agattcctag tgatcaaagc atcaccaatg 6464  
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Gly Lys Asp Gly Trp Val Pro Thr Pro Ser Glu Asp Tyr Ser His Trp
          35          40          45
Ser His Arg Asn Arg Phe Gln Val Asn Asp Thr Leu His Phe Lys Tyr
          50          55          60
Ala Lys Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn
          65          70          75          80
Thr Cys Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser
          85          90          95
Leu Phe Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn
          100          105          110
Ser Gln Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser
          115          120          125

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Thr Val His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser  
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 Pro Val His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu  
 145 150 155 160  
 Pro Ser Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr  
 165 170 175  
 Ala Pro Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu Val  
 180 185 190  
 Val Asn Ser Ile Ile Lys Pro Ile Asp Ser Phe Leu Leu Lys Ser Leu  
 195 200 205  
 Pro Leu Val Val Asp Val Ala Val Gly Ile Ser Thr Ser Arg Gln Leu  
 210 215 220  
 Gln Ala Ser Glu Glu Pro Val Ser Ser Pro Leu Ser Ser Pro Ala Leu  
 225 230 235 240  
 Leu Gly Ser Gly Lys Glu Glu Glu Gln Lys Ile Ile Pro Lys Arg Gln  
 245 250 255  
 Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val  
 260 265 270  
 Asn Leu Val Ala Ala Leu Val Arg Gly Met Arg Val Glu Asp Ala Leu  
 275 280 285  
 Ile Gln Leu Gln Val Thr Val Lys Arg Ala Ala Gln Thr Val Tyr Arg  
 290 295 300  
 Val Ile His Ala Ala Arg Ala Asn Ala Thr His Asn His Gly Leu Asp  
 305 310 315 320  
 Pro Asp Arg Leu Leu Val Ala Glu Ala Phe Val Gly Lys Gly Leu Phe  
 325 330 335  
 Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile Ser  
 340 345 350  
 Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro Glu  
 355 360 365  
 Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys Lys  
 370 375 380  
 Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser  
 385 390 395 400  
 Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu  
 405 410 415  
 Leu Val Leu Thr Ile Ile Leu Asp Val Thr Cys Val Gly Asn Met Glu  
 420 425 430



Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His  
           435                                  440                                  445  
 Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile  
           450                                  455                                  460  
 Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val  
           465                                  470                                  475                                  480  
 Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr  
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 Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg  
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 tac gca gcc act tgt ctc tcc gtc gaa gac gcc gtc aac gct cga tca 100  
 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser  
   10                                  15                                  20                                  25  
 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148  
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro  
                                   30                                  35                                  40  
 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196  
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys  
                                   45                                  50                                  55  
 tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244  
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser  
                                   60                                  65                                  70  
 tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292  
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser  
                                   75                                  80                                  85  
 acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340  
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser  
   90                                  95                                  100                                  105  
 tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388

Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp  
 110 115 120  
 atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg 436  
 Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser  
 125 130 135  
 gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac 484  
 Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His  
 140 145 150  
 aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg 532  
 Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp  
 155 160 165  
 aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta 580  
 Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu  
 170 175 180 185  
 ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act 628  
 Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr  
 190 195 200  
 gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa 676  
 Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu  
 205 210 215  
 gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga 718  
 Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala  
 220 225 230  
 aggtgtaaac t 729

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 <212> PRT  
 <213> Arabidopsis thaliana

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 Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe  
 35 40 45  
 Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly  
 50 55 60  
 Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu  
 65 70 75 80  
 Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr  
 85 90 95

Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala  
                   100                                  105                                  110  
 Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met  
                   115                                  120                                  125  
 Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala  
                   130                                  135                                  140  
 Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val  
                   145                                  150                                  155                                  160  
 Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg  
                   165                                  170                                  175  
 Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val  
                   180                                  185                                  190  
 His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp  
                   195                                  200                                  205  
 Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys  
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 Ala Ile Glu Glu Glu Ala  
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 <213> Arabidopsis thaliana

<220>  
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 <222> (12)..(1193)

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                   1                                  5                                  10  
 cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98  
 Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro  
                   15                                  20                                  25  
 agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146  
 Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys  
                   30                                  35                                  40                                  45  
 tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194  
 Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr  
                   50                                  55                                  60  
 cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
gtt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggg ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggg tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

290										295					300					
gca	cca	gtt	ttt	ata	tgt	ctc	ttg	gct	tta	cct	ttt	ttt	aaa	agt	atg	962				
Ala	Pro	Val	Phe	Ile	Cys	Leu	Leu	Ala	Leu	Pro	Phe	Phe	Lys	Ser	Met					
			305					310					315							
tat	gtg	cgt	agt	tca	agt	ttt	cga	ccg	att	cac	caa	gga	atg	ttt	tgg	1010				
Tyr	Val	Arg	Ser	Ser	Ser	Phe	Arg	Pro	Ile	His	Gln	Gly	Met	Phe	Trp					
		320					325					330								
ttg	ctt	ttg	gcg	gat	tgc	tta	cta	cta	ggg	tgg	atc	gga	tgt	caa	cct	1058				
Leu	Leu	Leu	Ala	Asp	Cys	Leu	Leu	Leu	Gly	Trp	Ile	Gly	Cys	Gln	Pro					
		335				340					345									
gtg	gag	gct	cca	ttt	gtt	act	att	gga	caa	att	tct	cct	ttg	gtt	ttc	1106				
Val	Glu	Ala	Pro	Phe	Val	Thr	Ile	Gly	Gln	Ile	Ser	Pro	Leu	Val	Phe					
350					355					360					365					
ttc	ttg	ttc	ttt	gcc	ata	acg	ccc	att	ctg	gga	cga	gtt	gga	aga	gga	1154				
Phe	Leu	Phe	Phe	Ala	Ile	Thr	Pro	Ile	Leu	Gly	Arg	Val	Gly	Arg	Gly					
				370					375					380						
att	cct	aat	tct	tac	acg	gat	gag	act	gat	cac	acc	tga	tcagt	gaaaa	1203					
Ile	Pro	Asn	Ser	Tyr	Thr	Asp	Glu	Thr	Asp	His	Thr									
			385					390												

&lt;210&gt; 46

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 46

Met	Thr	Ile	Arg	Asn	Gln	Arg	Phe	Ser	Leu	Leu	Lys	Gln	Pro	Ile	Ser
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Ser	Thr	Leu	Asn	Gln	His	Leu	Val	Asp	Tyr	Pro	Thr	Pro	Ser	Asn	Leu
			20					25					30		
Ser	Tyr	Trp	Trp	Gly	Phe	Gly	Pro	Leu	Ala	Gly	Ile	Cys	Leu	Val	Ile
		35					40					45			
Gln	Ile	Val	Thr	Gly	Val	Phe	Leu	Ala	Met	His	Tyr	Thr	Pro	His	Val
	50					55					60				
Asp	Leu	Ala	Phe	Asn	Ser	Val	Glu	His	Ile	Met	Arg	Asp	Val	Glu	Gly
65					70					75					80
Gly	Trp	Leu	Leu	Arg	Tyr	Met	His	Ala	Asn	Gly	Ala	Ser	Met	Phe	Leu
				85					90					95	
Ile	Val	Val	Tyr	Leu	His	Ile	Phe	Arg	Gly	Leu	Tyr	His	Ala	Ser	Tyr
			100					105					110		
Ser	Ser	Pro	Arg	Glu	Phe	Val	Trp	Cys	Leu	Gly	Val	Val	Ile	Phe	Leu
		115					120					125			

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln  
 130 135 140  
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile  
 145 150 155 160  
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser  
 165 170 175  
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu  
 180 185 190  
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His  
 195 200 205  
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys  
 210 215 220  
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val  
 225 230 235 240  
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val  
 245 250 255  
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro  
 260 265 270  
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu  
 275 280 285  
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val  
 290 295 300  
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg  
 305 310 315 320  
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu  
 325 330 335  
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala  
 340 345 350  
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe  
 355 360 365  
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn  
 370 375 380  
 Ser Tyr Thr Asp Glu Thr Asp His Thr  
 385 390

&lt;210&gt; 47

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1194)

&lt;400&gt; 47

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cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg	96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	
20 25 30	
caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt	144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	
35 40 45	
aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt	192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	
50 55 60	
att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt	240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	
65 70 75 80	
tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc	288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	
85 90 95	
aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc	336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	
100 105 110	
act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc	384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	
115 120 125	
gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat	432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	
130 135 140	
aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct	480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	
145 150 155 160	
agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg	528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	
165 170 175	
acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca	576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	
180 185 190	
gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att	624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	
195 200 205	

cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672  
 Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys  
 210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720  
 Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu  
 225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768  
 Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala  
 245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816  
 Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg  
 260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864  
 Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu  
 275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912  
 Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu  
 290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960  
 Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser  
 305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008  
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr  
 325 330 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056  
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu  
 340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104  
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu  
 355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152  
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser  
 370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194  
 Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn  
 385 390 395

&lt;210&gt; 48

&lt;211&gt; 397

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe



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Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	35	40	45
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	50	55	60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	65	70	75
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	85	90	95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	100	105	110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	115	120	125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	130	135	140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	145	150	155
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	165	170	175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	180	185	190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	195	200	205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys	210	215	220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu	225	230	235
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala	245	250	255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg	260	265	270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu	275	280	285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu	290	295	300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser			

305	310										315				320			
Pro	Cys	Ser	Ala	Ala	Lys	Ala	Asn	Leu	Ala	Thr	Tyr	Tyr	Phe	Ser	Thr			
				325					330					335				
Gly	Asp	Phe	Glu	Lys	Ser	Ile	Lys	Leu	Tyr	Glu	Glu	Pro	Met	Gly	Leu			
			340					345					350					
Lys	Asp	Thr	Asp	Lys	Ser	Tyr	Leu	Arg	Glu	Arg	Arg	Lys	Arg	Val	Glu			
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Ala	Thr	Thr	Leu	Arg	Ala	Pro	Phe	Val	Val	Gln	Leu	Thr	Val	Arg	Ser			
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gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct																						97
Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser																						
20																						30
cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att																						145
Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile																						
35																						45
agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg																						193
Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met																						
50																						60
act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg																						241
Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp																						
65																						75
ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc																						289
Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser																						
80																						95
tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc																						337
Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu																						
100																						110
																						105

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385  
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile  
                   115                  120                  125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433  
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val  
                   130                  135                  140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481  
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg  
                   145                  150                  155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529  
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr  
 160                  165                  170                  175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577  
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln  
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gaa tca caa aaa gac gag ctt taa agcaaagtcc 611  
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                   20                  25                  30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser  
                   35                  40                  45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr  
                   50                  55                  60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu  
                   65                  70                  75                  80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys  
                   85                  90                  95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala  
                   100                  105                  110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe  
                   115                  120                  125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys  
                   130                  135                  140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro  
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 Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala  
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 Ser Gln Lys Asp Glu Leu  
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 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro  
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 acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144  
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg  
 35 40 45  
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 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60  
 ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240  
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80  
 caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288  
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95  
 ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336  
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu  
 100 105 110  
 att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384  
 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys  
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr  
 355 360 365

gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152  
 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser  
 370 375 380

tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200  
 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys  
 385 390 395 400

aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248  
 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu  
 405 410 415

cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296  
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr  
 420 425 430

ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344  
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His  
 435 440 445

cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392  
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tag taa 1398

465

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 35 40 45

Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala  
 50 55 60

Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg  
 65 70 75 80

Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly  
 85 90 95

Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

100	105	110
Ile Gln Asp Gly Val Lys Ala	Ala Glu Glu Tyr Ala Lys Ser Gly Lys	
115	120	125
Val Pro Asp Pro Ser Cys Thr	Asp Asn Ala Glu Phe Gln Val Val Leu	
130	135	140
Ile Ile Ile Arg Glu Gly Leu Lys Thr	Asp Pro Leu Lys Tyr Thr Lys	
145	150	155
Arg Pro Ser Cys Leu Val Gly Val Ser	Glu Glu Thr Thr Thr Gly Val	
165	170	175
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr	Leu Leu Leu His Ala	
180	185	190
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile	Asp Asn Leu Tyr	
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Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met	Arg Ala Thr Asp Val	
210	215	220
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly	Asp Val Phe	
225	230	235
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg	Val Ile Val	
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Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met	Glu Gly Ser	
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Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val	Asp Arg Phe Val	
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Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp	His Met Arg Arg	
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Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe	Asp Asn Glu	
305	310	315
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys	Arg Ile Thr	
325	330	335
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr	Asn Arg Gly	
340	345	350
Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly	Cys Ala Thr	
355	360	365
Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr	Asn Gln Val Ser	
370	375	380
Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr	Glu Lys	
385	390	395
Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala	Leu	

	405		410		415
His Leu Val	Lys Leu Gly Ala Arg	Leu Thr Lys Leu Ser	Arg Cys Thr		
	420		425		430
Leu Leu Cys Thr Asp Asp Pro	Val Glu Gly Arg Lys	Glu Pro Pro His			
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Arg Ala Gly Ser Pro Glu Pro	Cys Gln Leu Gln Leu Thr Val Phe Arg				
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gac gtc gat gaa att gtc agg tta agg aag agg ttt ttc aag ttg gac	96
Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp	
20 25 30	
aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct	144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro	
35 40 45	
caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat	192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp	
50 55 60	
aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt	240
Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg	
65 70 75 80	
tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca	288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala	
85 90 95	
ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag	336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu	
100 105 110	
tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat	384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn	
115 120 125	
cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac	432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp	



130 135 140  
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 145 150 155 160  
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 Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly  
 165 170 175  
 gat gtg taa agttcagtcg accgtgaccg tgagcctgga agcctgaacg 577  
 Asp Val  
 ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637  
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 35 40 45  
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp  
 50 55 60  
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg  
 65 70 75 80  
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala  
 85 90 95  
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu  
 100 105 110  
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn  
 115 120 125  
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp  
 130 135 140  
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Asp Val

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<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

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<222> (10)..(1557)

<400> 55

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tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt 99  
 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val  
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tgc ttc gcc ggg gat ttt gat 147  
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp  
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tgc gat tgc gcc aag 195  
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys  
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243  
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg  
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291  
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp  
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339  
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp  
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387  
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp  
 115 120 125

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 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483  
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu  
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
240 245 250	
atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
255 260 265 270	
gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
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Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His  
 385 390 395  
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 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro  
 400 405 410  
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 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe  
 415 420 425 430  
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347  
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys  
 435 440 445  
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395  
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser  
 450 455 460  
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 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys  
 465 470 475  
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491  
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu  
 480 485 490  
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539  
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala  
 495 500 505 510  
 agc tcg ccc agg cgc tga taattaaatc cgatccgtcc tttaaccccc 1587  
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&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 56

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 20 25 30  
 Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp Ala Arg  
 35 40 45  
 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala  
 50 55 60

114

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro  
 65 70 75 80  
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg  
 85 90 95  
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly  
 100 105 110  
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe  
 115 120 125  
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr  
 130 135 140  
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val  
 145 150 155 160  
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro  
 165 170 175  
 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu  
 180 185 190  
 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp  
 195 200 205  
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser  
 210 215 220  
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser  
 225 230 235 240  
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu  
 245 250 255  
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys  
 260 265 270  
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp  
 275 280 285  
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala  
 290 295 300  
 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr  
 305 310 315 320  
 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys  
 325 330 335  
 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala  
 340 345 350  
 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile  
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr  
 370 375 380  
 Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu  
 385 390 395 400  
 Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr  
 405 410 415  
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser  
 420 425 430  
 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys  
 435 440 445  
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn  
 450 455 460  
 Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln  
 465 470 475 480  
 Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr  
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cgg gtg acc agg gac ggt tgg ggg ccc gga aaa acc ggt gtc aca cgc 99  
 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg  
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ggg tcg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147  
 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly  
 30 35 40 45

gca tcg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195  
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile  
 50 55 60

acg aca agc acc cgc gcg cgg cgc tac gcg gtc tcg gcc aaa ttc ccg	243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro	
65 70 75	
aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac	291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr	
80 85 90	
acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag	339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys	
95 100 105	
tta tta cct tcg aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa	387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu	
110 115 120 125	
tat tca att atg ttt ggt cca gat tcg aca ggt gca tca cgt act gtt	435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val	
130 135 140	
cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa	483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu	
145 150 155	
cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt	531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser	
160 165 170	
tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tcg	579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser	
175 180 185	
caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga	627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg	
190 195 200 205	
atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta	675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val	
210 215 220	
gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac	723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His	
225 230 235	
gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc	771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly	
240 245 250	
cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca	819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro	
255 260 265	
cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg	867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg	
270 275 280 285	

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915  
 Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr  
 290 295 300

cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963  
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala  
 305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011  
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met  
 320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059  
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr  
 335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107  
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly  
 350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155  
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu  
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aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203  
 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg  
 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251  
 Arg Thr Gly Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu  
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tac gga ccg gaa taa aatcgccctga tgcct 1281  
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&lt;210&gt; 58

&lt;211&gt; 417

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 58

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Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly Ala Ser Thr  
 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser  
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser  
 65 70 75 80



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				85					90					95	
Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	Leu	Leu	Pro
				100					105					110	
Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	Tyr	Ser	Ile
				115					120					125	
Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	Arg	Arg	Ala
				130					135					140	
Arg	Asn	Tyr	Lys	Gly	Lys	Arg	His	Leu	Arg	Lys	Lys	Glu	Gln	Asn	Lys
				145					150					155	160
Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	Trp	Ser	Pro
				165					170					175	
Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	Gln	Ala	Gly
				180					185					190	
Asn	Leu	Ala	Asp	Asp	Cys	Glu	Leu	Leu	Pro	Gln	Lys	Arg	Ile	Phe	Arg
				195					200					205	
Pro	Ser	Cys	Arg	Lys	Gln	Ser	Lys	Pro	Val	Thr	Cys	Val	Asp	Val	Lys
				210					215					220	
His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	Asp	Asp	Ile
				225					230					235	240
Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	Arg	Thr	Asn
				245					250					255	
Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	Arg	Pro	Arg
				260					265					270	
Arg	Tyr	Lys	Gly	Glu	Thr	Lys	Ala	Lys	Lys	His	Pro	Arg	Pro	Glu	Tyr
				275					280					285	
Lys	Gly	Thr	Trp	Val	Thr	Pro	Leu	Gln	Asp	Asn	Pro	Thr	Pro	Ala	Pro
				290					295					300	
Pro	Asn	Asp	Leu	Tyr	Leu	Phe	Leu	Asp	Leu	Gly	Ala	Ala	Gly	Thr	Arg
				305					310					315	320
Thr	Trp	Thr	Val	Lys	Ser	Gly	Ser	Ile	Thr	Asn	Asn	Met	Ile	Val	Thr
				325					330					335	
Thr	Ser	Val	Glu	Thr	Ala	Thr	Asp	Phe	Ser	Glu	Lys	Thr	Lys	Val	Ala
				340					345					350	
Asn	Thr	Thr	Thr	Glu	Leu	Asn	Asp	Gly	Arg	Asp	Ala	Gly	Thr	Gly	Ile
				355					360					365	
Gly	Ala	Glu	Arg	His	Cys	Ala	Asp	Glu	Arg	Trp	Lys	Glu	Thr	Thr	Val
				370					375					380	

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1 5 10 15	
aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca	96
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr	
20 25 30	
gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac	144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn	
35 40 45	
ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg	192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met	
50 55 60	
aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc	240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe	
65 70 75 80	
gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg	288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val	
85 90 95	
atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg	336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met	
100 105 110	
atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag	384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu	
115 120 125	
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Phe Val Lys Ile Met Met Ala Lys	
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             20                    25                    30  
 Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn  
             35                    40                    45  
 Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met  
     50                    55                    60  
 Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe  
     65                    70                    75                    80  
 Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val  
             85                    90                    95  
 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met  
             100                    105                    110  
 Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu  
             115                    120                    125  
 Phe Val Lys Ile Met Met Ala Lys  
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Asn Ser Ser Leu Ser Ser Gly Asn Gly Thr Glu Val Ala Thr Asp Val  
10 15 20

tct tct tgc ttc tat gtt ccc aat ccc tct gga acc gat ttc gat gcc 150  
Ser Ser Cys Phe Tyr Val Pro Asn Pro Ser Gly Thr Asp Phe Asp Ala  
25 30 35

gag tcg tct tct ctt cct cct ct gtaagtcttc tttgaatttt taaaaacatt 203  
Glu Ser Ser Ser Leu Pro Pro Le  
40 45

caactctcttg ctgctgtctc tgttgatcct tcttctttga aaatttgaaa acattcttag 263

tctctcgcgc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315  
u Ser Pro Ala Pro Gln Val Ala Leu Ser Ile Pro  
50 55

gcg gag ctt gcc gcc gcc att ccc ctc atc gat cgc ttc cag gtt gaa 363  
Ala Glu Leu Ala Ala Ala Ile Pro Leu Ile Asp Arg Phe Gln Val Glu  
60 65 70

gct ttt ctg cgg cta atg cag aaa caa atc cag tct gct ggg aag cgt 411  
Ala Phe Leu Arg Leu Met Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg  
75 80 85 90

ggc ttc ttc tat tcc aaa aag tcc tct ggc tcc aat gtc cgc gag cgc 459  
Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg  
95 100 105

ttc aca ttt gag gat atg ctt tgc ttt caa aag gtttttcttt ccccccttt 512  
Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys  
110 115

cttccccatt gacaatccat tgactg aat atg tct ctc tcc cct tcc ttc ctt 565  
Asn Met Ser Leu Ser Pro Ser Phe Leu  
120 125

cag gat cca atc ccc aca tct ctc ctc aag att aac agc gat ctc gtc 613  
Gln Asp Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val  
130 135 140

agc cgt gct acc aag ttg ttt cat ctc atc tta aaa tat atg ggt gtt	661
Ser Arg Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val	
145 150 155	
gat tca tct gat cga tct acg cct ccc agt tta gat gaa cgc att gac	709
Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp	
160 165 170	
ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg	757
Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg	
175 180 185 190	
gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac	805
Asp Glu Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp	
195 200 205	
agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc	853
Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser	
210 215 220	
tct atg cct cct agc aaa gat atc ggt gga tat cta tct gag tat att	901
Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile	
225 230 235	
cat aat gtc gca cac gat gca act att gaa ccg gat gct cag gtt ctt	949
His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu	
240 245 250	
gct gtt aac act ttg aaa gct tta aag cgc tct atc aaa gct ggt cct	997
Ala Val Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro	
255 260 265 270	
agg cac acc aca cct ggt cgt gaa gaa att gaa gcc ctt ttg acc ggt	1045
Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly	
275 280 285	
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Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu	
290 295 300	
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Ile Ser Tyr Asp Met Ala Thr Val Ser Asp Ala Val Glu	
305 310 315	
gtatcttctt gctttctttt ttcataattt accgctgac atattcttgt ccctttttct	1195
ctcactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca	1247
Leu Ala Gly Thr Ile Lys Leu Ser	
320	
gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt	1295
Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys Val Val Ser Ser	
325 330 335 340	
tct aaa tca tct gat ccc gga aat g gtatgctttc atatgactgg	1340
Ser Lys Ser Ser Asp Pro Gly Asn G	

345

cttcgtcata tattgtgaag taatacaaca ttatcgatca tttttctatc tgtgcacttg 1400

cag ag gaa tat ata gga ttg gat gat aac aag tat att gga gat ctc 1447  
 lu Glu Tyr Ile Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu  
 350 355 360

ctc gca gaa ttt aaa gct att aaa gac cga aat aaa gga gag ata cta 1495  
 Leu Ala Glu Phe Lys Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu  
 365 370 375

cac tgc aaa ctg gta ttt aaa aaa aaa tta ttc cga gag tct gat gaa 1543  
 His Cys Lys Leu Val Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu  
 380 385 390 395

gct gta aca gat ctg atg ttt gtg caa ctt tcg tat gtt caa 1585  
 Ala Val Thr Asp Leu Met Phe Val Gln Leu Ser Tyr Val Gln  
 400 405

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gacacacata tatgcag ctg caa cat gac tat ttg cta gga aac tat cct 1695  
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 Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu Gln Ile Leu Val  
 425 430 435

ggg att ggg ttt gtc aat agt cca gag tca tgc at gttagttttc 1788  
 Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Il  
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ttaagctccg ccattgactt tatttttagtt gtccgatact ttatttttcc aatttttctc 1848

ccttaacaat atcatttctt ttctcaatgt atcacatata ag t gat tgg aca tca 1903  
 e Asp Trp Thr Ser  
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ctt ctt gag cgg ttt ttg cca aga caa ata gca ata acc cga gca aag 1951  
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 455 460 465

cgt gaa tgg gaa ttg gat atc ctt gct cgc tac cgt tca atg 1993  
 Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg Ser Met  
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aaaccattg aagtgatggc atggtaaaat gatatttcgt atgtgtatgt gggcatgtag 2113

gag aac gtg acc aaa gat gat gca aga caa caa ttt cta cgg ata ctg 2161  
 Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg Ile Leu  
 485 490 495

aag gca ctg cca tac ggg aat tca gtt ttt ttt agc gta cgc aag ata 2209

125

Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile  
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 Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly Ile Asn  
 515 520 525 530  
 aaa cgt ggg gttgtctcaa tataaatgtt atacattatg actttaaaaa 2306  
 Lys Arg Gly  
 aactgttatt gttgtttgga attcaaactt atgttggttg atttgaattt gttgtttgct 2366  
 ttctttagtag gtt cac ttt ttt cga ccg gtt cct aaa gaa tat ctg cac tct 2417  
 Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr Leu His Ser  
 535 540 545  
 gct gaa cta cgt gac atc atg caa ttt ggc agc agt aac act gct gtc 2465  
 Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn Thr Ala Val  
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 Gly Glu Glu Ile  
 585  
 tgt gtt gct ttg caa aca cat ata aat gat gtc atg ttg cgt cgt tac 2667  
 Cys Val Ala Leu Gln Thr His Ile Asn Asp Val Met Leu Arg Arg Tyr  
 590 595 600  
 tcc aaa gct cga tct gct gcc aat tgc ttg gtt aat gga gat att tct 2715  
 Ser Lys Ala Arg Ser Ala Ala Asn Cys Leu Val Asn Gly Asp Ile Ser  
 605 610 615  
 tgt tgt tct aag ccg caa aat ttt gaa gtg tat gaa aaa cgt ttg caa 2763  
 Cys Cys Ser Lys Pro Gln Asn Phe Glu Val Tyr Glu Lys Arg Leu Gln  
 620 625 630  
 gat ttg tct aag gct tat gaa gag tcc caa aag aag att gag aag 2808  
 Asp Leu Ser Lys Ala Tyr Glu Glu Ser Gln Lys Lys Ile Glu Lys  
 635 640 645  
 gtacacattc taacaaattt cttatttatt cttcaatgta aaattgaata taatagaggg 2868  
 aggtgatct ttgtttaaat acatgaaata acttattgta gttggatttt ttcattggtt 2928  
 ttatgcttgg tagtcttgag atatttcagt atatatcacc ctctatctt atgttattgt 2988  
 atgtagaatg ttataccatg acctcttttg ttttagagtg gcatgctgat gaactattcg 3048  
 tatgttttat gttgttgat ag ttg atg gat gaa caa caa gag aaa aat cag 3100



Leu Met Asp Glu Gln Gln Glu Lys Asn Gln  
 650 655

caa gaa gtt act ctg cgt gaa gag tta gaa gct ata cac aat ggt ttg 3148  
 Gln Glu Val Thr Leu Arg Glu Glu Leu Glu Ala Ile His Asn Gly Leu  
 660 665 670 675

gag ctt gaa agg aga aaa ttg ttg gag gtt act tta gac cga gat aaa 3196  
 Glu Leu Glu Arg Arg Lys Leu Leu Glu Val Thr Leu Asp Arg Asp Lys  
 680 685 690

ctt agg tca ttg tgt gac gag aag gga acc cct att caa gtttagttata 3245  
 Leu Arg Ser Leu Cys Asp Glu Lys Gly Thr Pro Ile Gln  
 695 700

acctaacttt tgtctttctt ttgatgcttg gttgaagtta tttaatgatt tattctatat 3305

atgctatag tcc ttg atg tct gaa ctg cga gga atg gaa gca agg ttg gca 3356  
 Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala  
 705 710 715

aag tcg ggc aac acc aaa tca agt aaa gag acc aaa tca gaa tta gcc 3404  
 Lys Ser Gly Asn Thr Lys Ser Ser Lys Glu Thr Lys Ser Glu Leu Ala  
 720 725 730

gaa atg aat aat cag gtgaatatta tgtgtttaaa tctaattcat tgtaatcatt 3459  
 Glu Met Asn Asn Gln  
 735

gagttgttgt tttttgttcc caattctgct ttcctttgac aatgaatttt aagtcacag 3518

ata tta tac aag atc caa aag gag tta gaa gtt cga aat aag gaa ttg 3566  
 Ile Leu Tyr Lys Ile Gln Lys Glu Leu Glu Val Arg Asn Lys Glu Leu  
 740 745 750 755

cat gtc gca gtt gat aat tca aag agg ttg ttg agt gaa aac aag ata 3614  
 His Val Ala Val Asp Asn Ser Lys Arg Leu Leu Ser Glu Asn Lys Ile  
 760 765 770

ttg gag caa aat ctc aat att gaa aag aag aaa aaa gag gag 3656  
 Leu Glu Gln Asn Leu Asn Ile Glu Lys Lys Lys Lys Glu Glu  
 775 780 785

gtgaattcta tgtattagat ttattgaaga tttcaaattg agaagtatca aatacttgcg 3716

tattgttgac atctcattat ttcag gtt gaa att cat caa aag aga tat gaa 3768  
 Val Glu Ile His Gln Lys Arg Tyr Glu  
 790

caa gaa aaa aag gtg tta aag ctt cga gtt tct gaa ctt gaa aat aag 3816  
 Gln Glu Lys Lys Val Leu Lys Leu Arg Val Ser Glu Leu Glu Asn Lys  
 795 800 805 810

ctt gaa gta ctt gct caa gac ttg gat agt gct gag tct acg att gaa 3864  
 Leu Glu Val Leu Ala Gln Asp Leu Asp Ser Ala Glu Ser Thr Ile Glu  
 815 820 825

agt aag aat tct gac atg ctg ctg ttg caa aat aac ttg aaa gaa ctt 3912  
 Ser Lys Asn Ser Asp Met Leu Leu Leu Gln Asn Asn Leu Lys Glu Leu  
                     830                                    835                                    840

gag gag tta aga gaa atg aaa gag gtaatggtac tcttttgtct tcttcattat 3966  
 Glu Glu Leu Arg Glu Met Lys Glu  
                     845                                    850

ttaattttgt ttctgtttga atgatgataa tgtatttttcg cgattccaaa ttgaagtaga 4026

gggatgtgtt tacattccaa tttcattttc ttag gac att gac aga aaa aat gag 4081  
   Asp Ile Asp Arg Lys Asn Glu  
   855

caa aca gct gcc att ttg aaa atg caa gga gcc caa ctt gct gag cta 4129  
 Gln Thr Ala Ala Ile Leu Lys Met Gln Gly Ala Gln Leu Ala Glu Leu  
                     860                                    865                                    870

gaa ata ctt tat aag gaa gaa caa gtt tta agg aaa aga tac tat aat 4177  
 Glu Ile Leu Tyr Lys Glu Glu Gln Val Leu Arg Lys Arg Tyr Tyr Asn  
                     875                                    880                                    885

acc ata gaa g gtaacataat gctcaagtat gtacaatgat gttcattgct 4227  
 Thr Ile Glu A  
 890

tttaaaaaag aattttacta acattttttat ttgattgtag at atg aaa ggg aag 4281  
   sp Met Lys Gly Lys  
   895

att aga gtt tat tgt cga ata aga cct cta aat gaa aaa gag agt tca 4329  
 Ile Arg Val Tyr Cys Arg Ile Arg Pro Leu Asn Glu Lys Glu Ser Ser  
                     900                                    905                                    910

gag agg gaa aaa caa atg ctg aca act gtg gat gag ttt act gtt gaa 4377  
 Glu Arg Glu Lys Gln Met Leu Thr Thr Val Asp Glu Phe Thr Val Glu  
                     915                                    920                                    925

cat gca tgg aaa gac gac aaa aga aag caa cac ata tat gat cgc gta 4425  
 His Ala Trp Lys Asp Asp Lys Arg Lys Gln His Ile Tyr Asp Arg Val  
                     930                                    935                                    940                                    945

ttt gac atg cgt gct agt caa gat gat atc ttt gaa gac aca aag 4470  
 Phe Asp Met Arg Ala Ser Gln Asp Asp Ile Phe Glu Asp Thr Lys  
                     950                                    955                                    960

gtattattga tatgtaactg tgttcattta cctttcatcc tttgttattt tcttgtggtt 4530

actaacatcg ttttcctttt aacag tat ttg gta cag tcg gct gta gat ggg 4582  
   Tyr Leu Val Gln Ser Ala Val Asp Gly  
   965

tat aac gtt tgc atc ttt gca tat ggt caa act ggt tct gga aaa act 4630  
 Tyr Asn Val Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser Gly Lys Thr  
                     970                                    975                                    980                                    985

ttc act ata tat ggg cat gag agc aat cct gga ctc aca cct cga gct 4678

Phe Thr Ile Tyr Gly His Glu Ser Asn Pro Gly Leu Thr Pro Arg Ala  
 990 995 1000  
 aca aag gaa ctg ttc aac ata tta aag cga gat agc aag aga ttt tca 4726  
 Thr Lys Glu Leu Phe Asn Ile Leu Lys Arg Asp Ser Lys Arg Phe Ser  
 1005 1010 1015  
 ttt tct cta aag gtaatttggt atcctaataag atgatgtgat aaaagattat 4778  
 Phe Ser Leu Lys  
 1020  
 gacatcaact gactacaaaa agttatgcag gca tat atg gtg gaa ctt tat caa 4832  
 Ala Tyr Met Val Glu Leu Tyr Gln  
 1025  
 gac aca ctt gta gac ctt ttg tta cca aaa agt gca aga cgc ttg aaa 4880  
 Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser Ala Arg Arg Leu Lys  
 1030 1035 1040 1045  
 cta gag att aaa aaa gat tca aag gtattgtgag atatatctat tttaactagg 4934  
 Leu Glu Ile Lys Lys Asp Ser Lys  
 1050  
 ttataactag attgtagaca cgtaagtttg atcttatgca taaaatattt tctcag gga 4993  
 Gly  
 atg gtc ttt gta gag aat gtg aca act att cct ata tca act ttg gag 5041  
 Met Val Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu  
 1055 1060 1065 1070  
 gaa ctg cga atg att ctt gaa cgg gga tcg gaa cga cga cat gtt tct 5089  
 Glu Leu Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser  
 1075 1080 1085  
 gga aca aat atg aat gaa gaa agc tca aga tct cac ctc ata tta tca 5137  
 Gly Thr Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser  
 1090 1095 1100  
 gtt gtt att gaa agt att gat ctt caa acc cag tct gct gcg agg ggc 5185  
 Val Val Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly  
 1105 1110 1115  
 aag gtgacaaaat tcactatggt tttcttttatt gactcattat cattttttcac 5238  
 Lys  
 aggatttagt agcatttagg gattttaagg aaataggagt ttcttttagat tttcatgctt 5298  
 agtctaccga agaaaaatat agtaacatta atcttggtta agagagatat tatttttacag 5358  
 ctcaaattctt tgggtctggt caaaatgtta aacctttatg tacacaatcc atattattag 5418  
 tcaatgatat gccctccatt gttaaaccga tatcacctga tcatgggtggt atcttctaca 5478  
 atattctgaa tttttgtttg ttatttgcag ctg agt ttt gtg gat ctt gct ggt 5532  
 Leu Ser Phe Val Asp Leu Ala Gly  
 1120 1125

tct gag aga gtt aaa aag tcg ggc tca gct ggt tgc caa ctc aaa gaa 5580  
 Ser Glu Arg Val Lys Lys Ser Gly Ser Ala Gly Cys Gln Leu Lys Glu  
 1130 1135 1140

gct caa agt atc aac aaa tca ctt tct gca tta ggt gat gtt att ggt 5628  
 Ala Gln Ser Ile Asn Lys Ser Leu Ser Ala Leu Gly Asp Val Ile Gly  
 1145 1150 1155

gct tta tct tct ggc aac cag cat att cct tat agg aat cac aag cta 5676  
 Ala Leu Ser Ser Gly Asn Gln His Ile Pro Tyr Arg Asn His Lys Leu  
 1160 1165 1170 1175

acg atg ttg atg agc gat tca ttg ggc ggc aat gcc aag acg tta atg 5724  
 Thr Met Leu Met Ser Asp Ser Leu Gly Gly Asn Ala Lys Thr Leu Met  
 1180 1185 1190

ttt gtt aat gtg tct cca gcc gaa tca aat ttg gac gag acg tac aat 5772  
 Phe Val Asn Val Ser Pro Ala Glu Ser Asn Leu Asp Glu Thr Tyr Asn  
 1195 1200 1205

tct ctt ct gtaagtcacg agttcccata tatatataac ataaatcaaa tatgcttagt 5830  
 Ser Leu Le

gtaaaaatgg ataatccata ttgttttttt ttccctccttt gattccag a tat gca 5885  
 u Tyr Ala  
 1210

tcg aga gtg aga acg atc gtg aat gat ccc agc aaa cat ata tca tcc 5933  
 Ser Arg Val Arg Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser  
 1215 1220 1225

aaa gag atg gtg cga ttg aag aag ttg gta gca tac tgg aaa gag caa 5981  
 Lys Glu Met Val Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln  
 1230 1235 1240

gcc ggt aaa aaa ggt gag gaa gaa gac ttg gtg gat att gag gaa gat 6029  
 Ala Gly Lys Lys Gly Glu Glu Asp Leu Val Asp Ile Glu Glu Asp  
 1245 1250 1255 1260

cgt aca cga aaa gat gag gca gat agt tga agaaagctga c 6070  
 Arg Thr Arg Lys Asp Glu Ala Asp Ser  
 1265 1270

&lt;210&gt; 62

&lt;211&gt; 1269

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 62

Met Glu Gly Gln Arg Gly Ser Asn Ser Ser Leu Ser Ser Gly Asn Gly  
 1 5 10 15

Thr Glu Val Ala Thr Asp Val Ser Ser Cys Phe Tyr Val Pro Asn Pro  
 20 25 30

Ser Gly Thr Asp Phe Asp Ala Glu Ser Ser Ser Leu Pro Pro Leu Ser

35                                      40                                      45  
 Pro Ala Pro Gln Val Ala Leu Ser Ile Pro Ala Glu Leu Ala Ala Ala  
     50                                      55                                      60  
 Ile Pro Leu Ile Asp Arg Phe Gln Val Glu Ala Phe Leu Arg Leu Met  
     65                                      70                                      75                                      80  
 Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg Gly Phe Phe Tyr Ser Lys  
                                     85                                      90                                      95  
 Lys Ser Ser Gly Ser Asn Val Arg Glu Arg Phe Thr Phe Glu Asp Met  
                                     100                                      105                                      110  
 Leu Cys Phe Gln Lys Asn Met Ser Leu Ser Pro Ser Phe Leu Gln Asp  
                                     115                                      120                                      125  
 Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val Ser Arg  
     130                                      135                                      140  
 Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val Asp Ser  
     145                                      150                                      155                                      160  
 Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp Leu Val  
                                     165                                      170                                      175  
 Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg Asp Glu  
                                     180                                      185                                      190  
 Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp Arg Gln  
                                     195                                      200                                      205  
 Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser Ser Met  
     210                                      215                                      220  
 Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile His Asn  
     225                                      230                                      235                                      240  
 Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu Ala Val  
                                     245                                      250                                      255  
 Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro Arg His  
                                     260                                      265                                      270  
 Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly Arg Lys  
     275                                      280                                      285  
 Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu Ile Ser  
     290                                      295                                      300  
 Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu Leu Ala Gly Thr  
     305                                      310                                      315                                      320  
 Ile Lys Leu Ser Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys  
                                     325                                      330                                      335  
 Val Val Ser Ser Ser Lys Ser Ser Asp Pro Gly Asn Glu Glu Tyr Ile

340 345 350  
 Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu Leu Ala Glu Phe Lys  
 355 360 365  
 Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu His Cys Lys Leu Val  
 370 375 380  
 Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu Ala Val Thr Asp Leu  
 385 390 395 400  
 Met Phe Val Gln Leu Ser Tyr Val Gln Leu Gln His Asp Tyr Leu Leu  
 405 410 415  
 Gly Asn Tyr Pro Val Gly Arg Asp Asp Ala Ala Gln Leu Cys Ala Leu  
 420 425 430  
 Gln Ile Leu Val Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Ile  
 435 440 445  
 Asp Trp Thr Ser Leu Leu Glu Arg Phe Leu Pro Arg Gln Ile Ala Ile  
 450 455 460  
 Thr Arg Ala Lys Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg  
 465 470 475 480  
 Ser Met Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg  
 485 490 495  
 Ile Leu Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg  
 500 505 510  
 Lys Ile Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly  
 515 520 525  
 Ile Asn Lys Arg Gly Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr  
 530 535 540  
 Leu His Ser Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn  
 545 550 555 560  
 Thr Ala Val Phe Phe Lys Met Arg Val Ala Gly Val Leu His Ile Phe  
 565 570 575  
 Gln Phe Glu Thr Lys Gln Gly Glu Glu Ile Cys Val Ala Leu Gln Thr  
 580 585 590  
 His Ile Asn Asp Val Met Leu Arg Arg Tyr Ser Lys Ala Arg Ser Ala  
 595 600 605  
 Ala Asn Cys Leu Val Asn Gly Asp Ile Ser Cys Cys Ser Lys Pro Gln  
 610 615 620  
 Asn Phe Glu Val Tyr Glu Lys Arg Leu Gln Asp Leu Ser Lys Ala Tyr  
 625 630 635 640  
 Glu Glu Ser Gln Lys Lys Ile Glu Lys Leu Met Asp Glu Gln Gln Glu

645										650					655				
Lys	Asn	Gln	Gln	Glu	Val	Thr	Leu	Arg	Glu	Glu	Leu	Glu	Ala	Ile	His				
			660					665						670					
Asn	Gly	Leu	Glu	Leu	Glu	Arg	Arg	Lys	Leu	Leu	Glu	Val	Thr	Leu	Asp				
		675					680					685							
Arg	Asp	Lys	Leu	Arg	Ser	Leu	Cys	Asp	Glu	Lys	Gly	Thr	Pro	Ile	Gln				
	690					695					700								
Ser	Leu	Met	Ser	Glu	Leu	Arg	Gly	Met	Glu	Ala	Arg	Leu	Ala	Lys	Ser				
705					710					715					720				
Gly	Asn	Thr	Lys	Ser	Ser	Lys	Glu	Thr	Lys	Ser	Glu	Leu	Ala	Glu	Met				
				725					730					735					
Asn	Asn	Gln	Ile	Leu	Tyr	Lys	Ile	Gln	Lys	Glu	Leu	Glu	Val	Arg	Asn				
			740					745					750						
Lys	Glu	Leu	His	Val	Ala	Val	Asp	Asn	Ser	Lys	Arg	Leu	Leu	Ser	Glu				
		755					760					765							
Asn	Lys	Ile	Leu	Glu	Gln	Asn	Leu	Asn	Ile	Glu	Lys	Lys	Lys	Lys	Glu				
	770					775					780								
Glu	Val	Glu	Ile	His	Gln	Lys	Arg	Tyr	Glu	Gln	Glu	Lys	Lys	Val	Leu				
785					790					795					800				
Lys	Leu	Arg	Val	Ser	Glu	Leu	Glu	Asn	Lys	Leu	Glu	Val	Leu	Ala	Gln				
				805					810					815					
Asp	Leu	Asp	Ser	Ala	Glu	Ser	Thr	Ile	Glu	Ser	Lys	Asn	Ser	Asp	Met				
			820					825					830						
Leu	Leu	Leu	Gln	Asn	Asn	Leu	Lys	Glu	Leu	Glu	Glu	Leu	Arg	Glu	Met				
		835					840					845							
Lys	Glu	Asp	Ile	Asp	Arg	Lys	Asn	Glu	Gln	Thr	Ala	Ala	Ile	Leu	Lys				
	850					855					860								
Met	Gln	Gly	Ala	Gln	Leu	Ala	Glu	Leu	Glu	Ile	Leu	Tyr	Lys	Glu	Glu				
865					870					875					880				
Gln	Val	Leu	Arg	Lys	Arg	Tyr	Tyr	Asn	Thr	Ile	Glu	Asp	Met	Lys	Gly				
				885					890					895					
Lys	Ile	Arg	Val	Tyr	Cys	Arg	Ile	Arg	Pro	Leu	Asn	Glu	Lys	Glu	Ser				
			900					905					910						
Ser	Glu	Arg	Glu	Lys	Gln	Met	Leu	Thr	Thr	Val	Asp	Glu	Phe	Thr	Val				
		915					920					925							
Glu	His	Ala	Trp	Lys	Asp	Asp	Lys	Arg	Lys	Gln	His	Ile	Tyr	Asp	Arg				
	930					935					940								
Val	Phe	Asp	Met	Arg	Ala	Ser	Gln	Asp	Asp	Ile	Phe	Glu	Asp	Thr	Lys				

945                      950                      955                      960  
 Tyr Leu Val Gln Ser Ala Val Asp Gly Tyr Asn Val Cys Ile Phe Ala  
                                  965                      970                      975  
 Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu  
                                  980                      985                      990  
 Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile  
                                  995                      1000                      1005  
 Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met  
                                  1010                      1015                      1020  
 Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser  
 025                      1030                      1035                      1040  
 Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val  
                                  1045                      1050                      1055  
 Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu  
                                  1060                      1065                      1070  
 Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr  
                                  1075                      1080                      1085  
 Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val  
                                  1090                      1095                      1100  
 Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly Lys Leu  
 105                      1110                      1115                      1120  
 Ser Phe Val Asp Leu Ala Gly Ser Glu Arg Val Lys Lys Ser Gly Ser  
                                  1125                      1130                      1135  
 Ala Gly Cys Gln Leu Lys Glu Ala Gln Ser Ile Asn Lys Ser Leu Ser  
                                  1140                      1145                      1150  
 Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile  
                                  1155                      1160                      1165  
 Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly  
                                  1170                      1175                      1180  
 Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser  
 185                      1190                      1195                      1200  
 Asn Leu Asp Glu Thr Tyr Asn Ser Leu Leu Tyr Ala Ser Arg Val Arg  
                                  1205                      1210                      1215  
 Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser Lys Glu Met Val  
                                  1220                      1225                      1230  
 Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln Ala Gly Lys Lys  
                                  1235                      1240                      1245  
 Gly Glu Glu Glu Asp Leu Val Asp Ile Glu Glu Asp Arg Thr Arg Lys



1250

1255

1260

Asp Glu Ala Asp Ser  
265

&lt;210&gt; 63

&lt;211&gt; 2105

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1947)

&lt;400&gt; 63

atg aat aca gat aaa atg acc aag atg gat cta acg ggg tcc aat aac	48
Met Asn Thr Asp Lys Met Thr Lys Met Asp Leu Thr Gly Ser Asn Asn	
1 5 10 15	
gtg ccc att aat cca ccg acc act aag cgt gat ctt aga cag aat gat	96
Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp	
20 25 30	
aat aat aac cct aag agt cat aat agt cat aat agc aat ggg atg act	144
Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr	
35 40 45	
ggt aac agg aac aat aat aat aaa aat gcc ggc gga gtt gaa act agt	192
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser	
50 55 60	
aaa aaa gcg cgc tca cga ctg gaa aca cat ccc cga gat aat gag aat	240
Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn	
65 70 75 80	
aat tac aga cta gct aca agt gcc ggt acg aaa gga ggt gcg cga acc	288
Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr	
85 90 95	
gtt gac gta cca gtc ata tta agt acc cgg gaa tca caa ggc aca cgt	336
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg	
100 105 110	
tca gta aat gca aca agt aaa att aga tgc ccg gat tcc act gca att	384
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile	
115 120 125	
tgc gag tgg ttc gcc acg ccc acg gat cct caa aga cca gga gtt tat	432
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr	
130 135 140	
aac cac aag aac ggc gac aaa aac aac aga gat acc ggg aac att aat	480
Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn	
145 150 155 160	

acc gtt agc agt cta atg gat aat gct agg ggt ccg aac ccg cga tct	528
Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
165 170 175	
ggg att tca ata ccg aca cca acc tct aga caa tcc cca agt gag aca	576
Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
180 185 190	
cct cca gat cca ctg cag aat cct aat aat tat act agg tat cat aat	624
Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
195 200 205	
gat aaa aac agc aag aat agt aac aga aac tac aat aag aga aat aag	672
Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys	
210 215 220	
aac tcg acg acc ttt aat aac tcg gac ctt cct ggt cat aat aga agc	720
Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser	
225 230 235 240	
tcc cct gcg att aat gca gta aaa tca gca tca aat cga tca tct gct	768
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Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
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ccg gcg gac agc cga aaa tta gta gcg aat tct act tcc ttt cat cca 196

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 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr  
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Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu  
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aca atg att ggg aag ggt gca ttc gga gag gtaacatctc ttttatagat 256  
Thr Met Ile Gly Lys Gly Ala Phe Gly Glu  
50 55

catagtctgt tactctgttt tctcagcctc tcattggcat gcatcatctt gaaatgttct 316

ctgtgatgca tccttcttga aaggtcttct taggccattt tttttaccac agctaatttt 376

tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431  
Val Arg Ile Cys  
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agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479  
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys  
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Ser Glu Met Leu Arg Arg Gly Gln Val  
80 85

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Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631  
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn  
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Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro  
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Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn  
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 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu  
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 aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773  
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 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815  
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Arg	Gln	Arg	His	Lys	Met	Gly	Ala	Asp	Asp	Phe	Glu	Pro	Leu	Thr	Met	
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Ala	Glu	Val	Asp	Ser	Asn	Cys	Ile	Val	Lys	Leu	Tyr	Cys	Ser	Phe	Gln	
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His	Asn	Tyr	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp	
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Lys	Asp	Gly	His	Met	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Pro	Leu	

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Ser	Gly	Ala	Leu	Gln	Ser	Asp	Gly	Arg	Pro	Val	Ala	Thr	Arg	Arg	Thr				
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Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu				
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Gln	Met	Lys	Ala	Ala	Phe	Ile	Pro	Gln	Val	Asn	Asp	Glu	Leu	Asp	Thr				
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Phe	Val	Gly	Tyr	Thr	Tyr	Lys	Asn	Val	Glu	Ile	Val	Asn	Asp	Asp	Gln				
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gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
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Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
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cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
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Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
           125          130          135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
           140          145          150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
           155          160          165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
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Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
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Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
  65             70             75             80
Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
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Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
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Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp  
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 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp  
 145 150 155 160  
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu  
 165 170 175  
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly  
 180 185 190  
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr  
 195 200 205  
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser  
 210 215 220  
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys  
 225 230 235 240  
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 sp Ser Phe Gly Tyr Thr Thr Asp Glu  
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cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327  
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 80 85 90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519  
 Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val  
 95 100 105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567  
 Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu  
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gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615  
 Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His  
 125 130 135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660  
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 165 170 175

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 180 185 190

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr  
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 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser 225  
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 245 250  
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 275 280 285  
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 Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser  
 50 55 60  
 Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys  
 65 70 75 80  
 Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu  
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 Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln  
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Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly  
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                   145                                  150                                  155                                  160  
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 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser  
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 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser  
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 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr  
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 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly  
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 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp  
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 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro  
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Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
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Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
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Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
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Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
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Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
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Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
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Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
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tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tcg aaa tta gag gcg	579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

255	260	265	
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac			867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga			915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr			
350	355	360	
ggg gca gcg cca tga			1122
Gly Ala Ala Pro			
365			

&lt;210&gt; 76

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 76

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Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg	
35 40 45	
Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser	
50 55 60	
Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu	
65 70 75 80	
Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu	
85 90 95	
Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu	
100 105 110	

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu  
 115 120 125  
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu  
 130 135 140  
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val  
 145 150 155 160  
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp  
 165 170 175  
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp  
 180 185 190  
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val  
 195 200 205  
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu  
 210 215 220  
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu  
 225 230 235 240  
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg  
 245 250 255  
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser  
 260 265 270  
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro  
 275 280 285  
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg  
 290 295 300  
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro  
 305 310 315 320  
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys  
 325 330 335  
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr  
 340 345 350  
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro  
 355 360 365

&lt;210&gt; 77

&lt;211&gt; 1650

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

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                  1             5             10

ctt gag gga gat ttc aac aag gat aat act tct tct gca aca gaa att 101
Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile
                15             20             25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa 149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys
                30             35             40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc 197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala
                45             50             55

aat gcg gtaatat act tgaccctgct ttttcttttt ccttttcttt gttacaatgg 253
Asn Ala
60

gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac 308
                Asp Val Asp Val Cys Asn
                        65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac 356
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr
                70             75             80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat 404
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp
                85             90             95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att 452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile
100             105             110             115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct 502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly
                120             125

tacccaaaga agcataaaag caattcacta gcctgattct tctttcttct cctcttttgt 562

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actagtagca tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671  
Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe  
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719  
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro  
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767  
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr  
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815  
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala  
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868  
Leu Thr Ala Phe Ile Phe Gly Ar  
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044  
g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092  
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg  
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140  
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr  
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188  
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly  
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236  
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His  
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284  
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu  
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332  
Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly  
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380  
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile  
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428  
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg  
                   310                                  315                                  320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476  
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr  
                   325                                  330                                  335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524  
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile  
                   340                                  345                                  350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572  
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn  
                   355                                  360                                  365                                  370

cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625  
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ctttgtgaga ctattgccaa gttag 1650

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<212> PRT

<213> Arabidopsis thaliana

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                   20                                  25                                  30

Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu  
                   35                                  40                                  45

Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp  
                   50                                  55                                  60

Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu  
   65                                  70                                  75                                  80

Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe  
                   85                                  90                                  95

Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly  
                   100                                  105                                  110

Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp  
                   115                                  120                                  125

Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu  
                   130                                  135                                  140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala  
 145 150 155 160  
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser  
 165 170 175  
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe  
 180 185 190  
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu  
 195 200 205  
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn  
 210 215 220  
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr  
 225 230 235 240  
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp  
 245 250 255  
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu  
 260 265 270  
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile  
 275 280 285  
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val  
 290 295 300  
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys  
 305 310 315 320  
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn  
 325 330 335  
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile  
 340 345 350  
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<400> 79

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gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
              15                      20                      25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
              30                      35                      40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
              45                      50                      55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
              60                      65                      70                      75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
              80                      85                      90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
              95                      100                      105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
              110                      115                      120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
              125                      130                      135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
              140                      145                      150                      155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
              160                      165                      170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
              175                      180                      185

gaagattatc attaa
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&lt;210&gt; 80

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 80



Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln Glu Val Pro Lys Val  
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 20 25 30  
 Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile  
 35 40 45  
 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu  
 50 55 60  
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser  
 65 70 75 80  
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys  
 85 90 95  
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu  
 100 105 110  
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly  
 115 120 125  
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val  
 130 135 140  
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile  
 145 150 155 160  
 Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr  
 165 170 175  
 Val Glu Glu Glu Lys Lys Asp Lys Glu  
 180 185

&lt;210&gt; 81

&lt;211&gt; 1376

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (20)..(1366)

&lt;400&gt; 81

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 Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala  
 1 5 10  
 gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100  
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys  
 15 20 25  
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
		30					35					40					
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggg	gtg	ata	ggg	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
	60				65				70						75		
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
			95					100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggg	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
	110						115					120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
	125					130					135						
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
	140				145					150					155		
aag	acg	gcg	gag	aag	att	ggg	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
			160						165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
			175					180					185				
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
		190					195					200					
aag	gtt	ggg	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205					210				215							
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
	220				225					230					235		
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
			240					245						250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tgc ggg aag aca gag			868
Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu			
270	275	280	
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac			916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn			
285	290	295	
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga			964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg			
300	305	310	315
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag			1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu			
320	325	330	
gca tct caa aag act agg gag agt act gag tgc gga gct caa aaa gcc			1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala			
335	340	345	
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg			1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly			
350	355	360	
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa			1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys			
365	370	375	
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag			1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu			
380	385	390	395
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca			1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser			
400	405	410	
aag ccg ggt aag gtg gcg act tca ctg aag gcg tgc gat caa atg acc			1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr			
415	420	425	
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa			1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys			
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Asp Lys Gly Lys Leu			
445			

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 <400> 82

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 35 40 45  
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly  
 50 55 60  
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala  
 65 70 75 80  
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val  
 85 90 95  
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr  
 100 105 110  
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala  
 115 120 125  
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn  
 130 135 140  
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys  
 145 150 155 160  
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys  
 165 170 175  
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp  
 180 185 190  
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr  
 195 200 205  
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala  
 210 215 220  
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu  
 225 230 235 240  
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr  
 245 250 255  
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys  
 260 265 270  
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys  
 275 280 285  
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly  
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu  
 305 310 315 320  
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr  
 325 330 335  
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp  
 340 345 350  
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala  
 355 360 365  
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser  
 370 375 380  
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly  
 385 390 395 400  
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val  
 405 410 415  
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn  
 420 425 430  
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu  
 435 440 445

<210> 83  
 <211> 561  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (18) .. (548)

<400> 83

aaccacacaa atacaaa atg aat gaa atg tcg ttc ttt ggt tat agt ttc 50  
 Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe  
 1 5 10  
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98  
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr  
 15 20 25  
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146  
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln  
 30 35 40  
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194  
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly  
 45 50 55  
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242  
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

&lt;210&gt; 84

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp  
 115 120 125  
 Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg  
 130 135 140  
 Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val  
 145 150 155 160  
 Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr  
 165 170 175

<210> 85  
 <211> 988  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (12)..(977)

<400> 85  
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 Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe  
 1 5 10  
 tta gtt ttg ttg ttt gct caa gcc aat tcg caa ggt ttg aaa gta ggt 98  
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly  
 15 20 25  
 ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146  
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val  
 30 35 40 45  
 gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194  
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu  
 50 55 60  
 aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242  
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val  
 65 70 75  
 ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290  
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn  
 80 85 90  
 cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338  
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu  
 95 100 105  
 gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386  
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu  
 110 115 120 125

gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt	434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val	
130 135 140	
gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac	482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn	
145 150 155	
ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc	530
Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg	
160 165 170	
tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac	578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His	
175 180 185	
aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac	626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn	
190 195 200 205	
ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc	674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala	
210 215 220	
gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta	722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu	
225 230 235	
gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg	770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr	
240 245 250	
cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc	818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu	
255 260 265	
gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat	866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His	
270 275 280 285	
ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt	914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly	
290 295 300	
cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt	962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys	
305 310 315	
cgg tct gct aat taa gagatataga aa	989
Arg Ser Ala Asn	
320	

&lt;210&gt; 86

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana



&lt;400&gt; 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu  
 1 5 10 15  
 Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser  
 20 25 30  
 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp  
 35 40 45  
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe  
 50 55 60  
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp  
 65 70 75 80  
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu  
 85 90 95  
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val  
 100 105 110  
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg  
 115 120 125  
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly  
 130 135 140  
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser  
 145 150 155 160  
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly  
 165 170 175  
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly  
 180 185 190  
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly  
 195 200 205  
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu  
 210 215 220  
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp  
 225 230 235 240  
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala  
 245 250 255  
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser  
 260 265 270  
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met  
 275 280 285  
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

125

290

295

300

Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala  
 305 310 315 320

Asn

&lt;210&gt; 87

&lt;211&gt; 650

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (8) .. (634)

&lt;400&gt; 87

agcgaca atg gcg tcg att acg aac ctc gcc tct tct ctc tct tca ctc 49  
 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu  
 1 5 10

tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97  
 Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro  
 15 20 25 30

cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145  
 Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala  
 35 40 45

tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193  
 Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu  
 50 55 60

ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241  
 Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe  
 65 70 75

gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289  
 Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala  
 80 85 90

aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337  
 Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg  
 95 100 105 110

gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385  
 Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val  
 115 120 125

aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433  
 Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe  
 130 135 140

gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481  
 Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

145	150	155	
ttg gga gtc gca cgt gca ctc	ctg aag gta agt gca gac cac aga tcg		529
Leu Gly Val Ala Arg Ala Leu	Leu Lys Val Ser Ala Asp His Arg Ser		
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
	195	200	205
aag cgt taa gagttttata tatcat			650
Lys Arg			
<210> 88			
<211> 208			
<212> PRT			
<213> Arabidopsis thaliana			
<400> 88			
Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe			
1	5	10	15
Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala			
	20	25	30
Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu			
	35	40	45
Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val			
	50	55	60
Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala			
	65	70	75
			80
Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val			
	85	90	95
Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala			
	100	105	110
Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val			
	115	120	125
Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys			
	130	135	140
Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly			
	145	150	155
			160
Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu			
	165	170	175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys  
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg  
 195 200 205

<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

aacaagtgaa gcaca atg ggg atc atc gaa agg att aaa gaa atc gag gcc 51  
 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala  
 1 5 10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99  
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly  
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147  
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro  
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195  
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr  
 45 50 55 60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243  
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser  
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291  
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr  
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339  
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp  
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387  
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser  
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435  
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser  
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483  
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg  
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203  
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro  
                     385                    390                    395

ctt aag caa taa gcttttag 1223  
 Leu Lys Gln  
                     400

<210> 90

<211> 399

<212> PRT

<213> Arabidopsis thaliana

<400> 90

Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala Glu Met Ala Arg  
   1                    5                    10                    15  
 Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala  
                     20                    25                    30  
 Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala  
                     35                    40                    45  
 Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg  
   50                    55                    60  
 Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr  
   65                    70                    75                    80  
 Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr  
                     85                    90                    95  
 Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln  
                     100                    105                    110  
 Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly  
   115                    120                    125  
 Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu  
   130                    135                    140  
 Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr  
   145                    150                    155                    160  
 Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln  
                     165                    170                    175  
 Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr  
                     180                    185                    190  
 Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His  
   195                    200                    205  
 Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr  
   210                    215                    220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys  
 225 230 235 240  
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val  
 245 250 255  
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu  
 260 265 270  
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly  
 275 280 285  
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp  
 290 295 300  
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp  
 305 310 315 320  
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala  
 325 330 335  
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu  
 340 345 350  
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys  
 355 360 365  
 Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala  
 370 375 380  
 Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln  
 385 390 395

<210> 91  
 <211> 536  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (12)..(524)

<400> 91  
 aaataaaaac a atg aca agc tcc gat caa tct cca tcg cac gac gtc ttc 50  
                   Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe  
                   1                  5                  10  
 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98  
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu  
           15                  20                  25  
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146  
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr  
           30                  35                  40                  45

aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194  
 Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly  
                     50                                    55                                    60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242  
 Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu  
                     65                                    70                                    75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290  
 Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu  
                     80                                    85                                    90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338  
 Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val  
                     95                                    100                                    105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386  
 Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu  
 110                                    115                                    120                                    125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434  
 Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys  
                     130                                    135                                    140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482  
 Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe  
                     145                                    150                                    155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524  
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agaagttggt ta 536

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 <212> PRT  
 <213> Arabidopsis thaliana

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Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro  
                     20                                    25                                    30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys  
           35                                    40                                    45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn  
           50                                    55                                    60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp  
           65                                    70                                    75                                    80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu



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<211> 45  
 <212> PRT  
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 Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser  
                     20                    25                    30  
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys  
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 <222> (14)..(868)

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                     1                    5                    10  
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97  
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe  
             15                    20                    25  
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145  
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe  
             30                    35                    40  
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193  
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met  
             45                    50                    55                    60  
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241  
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val  
                     65                    70                    75  
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289  
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His  
                     80                    85                    90  
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337  
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser  
             95                    100                    105  
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385  
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser  
             110                    115                    120

aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433  
 Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser 140  
 125 130 135  
 cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481  
 His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly 155  
 145 150  
 gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529  
 Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val 170  
 160 165  
 gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577  
 Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu 185  
 175 180  
 tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625  
 Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr 200  
 190 195  
 ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673  
 Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu 220  
 205 210 215  
 gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721  
 Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val 235  
 225 230  
 aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769  
 Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe 250  
 240 245  
 aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817  
 Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu 265  
 255 260  
 aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865  
 Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu 280  
 270 275  
 tga acatcttttt tt 880  
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&lt;210&gt; 96

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 96

Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser  
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Leu Ala Leu Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro  
 20 25 30

Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser  
                   35                                  40  45  
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln  
           50                                  55  60  
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp  
   65                                  70  75                                  80  
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn  
                                   85  90  95  
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe  
                                   100  105  110  
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val  
                                   115  120  125  
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr  
   130                                  135  140  
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala  
   145                                  150  155                                  160  
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val  
                                   165  170  175  
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro  
                                   180  185  190  
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile  
                                   195  200  205  
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile  
   210                                  215  220  
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp  
   225                                  230  235                                  240  
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val  
                                   245  250  255  
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu  
                                   260  265  270  
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu  
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&lt;222&gt; (18)..(821)

&lt;400&gt; 97

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		1 5 10	
gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc	98		
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val			
		15 20 25	
ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag	146		
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys			
		30 35 40	
ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg	194		
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu			
		45 50 55	
ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc	242		
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro			
		60 65 70 75	
gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca	290		
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr			
		80 85 90	
ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg	338		
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met			
		95 100 105	
ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga	386		
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly			
		110 115 120	
gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc	434		
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe			
		125 130 135	
agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct	482		
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala			
		140 145 150 155	
cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc	530		
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala			
		160 165 170	
gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag	578		
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu			
		175 180 185	
gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc	626		
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr			
		190 195 200	
gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga	674		

Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly  
 205 210 215  
 aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722  
 Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val  
 220 225 230 235  
 act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770  
 Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro  
 240 245 250  
 gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818  
 Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 255 260 265  
 tga gccaaagtttt 831

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 35 40 45  
 Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly  
 50 55 60  
 Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp  
 65 70 75 80  
 Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg  
 85 90 95  
 Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly  
 100 105 110  
 Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu  
 115 120 125  
 Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu  
 130 135 140  
 Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala  
 145 150 155 160  
 Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg  
 165 170 175

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro  
 180 185 190  
 Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe  
 195 200 205  
 Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe  
 210 215 220  
 Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro  
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 Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys  
 260 265

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 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp  
 15 20 25  
 ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146  
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu  
 30 35 40  
 cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194  
 Pro Phe Ile Leu Arg Asn  
 45 50  
 atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301  
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile  
 55 60 65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt 355  
 Phe G

atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462  
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys  
 70 75 80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510  
 Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met  
 85 90 95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558  
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu  
 100 105 110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606  
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys  
 115 120 125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654  
 Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val  
 130 135 140 145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702  
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe  
 150 155 160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750  
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly  
 165 170 175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798  
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp  
 180 185 190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843  
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 195 200 205

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 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu  
                     35                    40                    45  
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys  
                     50                    55                    60  
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser  
                     65                    70                    75                    80  
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile  
                     85                    90                    95  
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser  
                     100                    105                    110  
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr  
                     115                    120                    125  
 Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu  
                     130                    135                    140  
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp  
                     145                    150                    155                    160  
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu  
                     165                    170                    175  
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser  
                     180                    185                    190  
 Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu  
                     195                    200                    205

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 1 5 10

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 Thr Ala Gly Lys Ala Gl  
 15

cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157  
 actagaaatt tcagttactt gtttaattta gtttgctgta attatgtaat tgatgatttt 217  
 atgggtacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268  
 u Glu Lys Ser Asn Val Leu Leu Asp Lys  
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319  
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl  
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379  
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432  
 n Ala Gly Lys Ser Val  
 45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480  
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly  
 50 55 60

ctg aac aag tag agattcgggt caaatttggg 512  
 Leu Asn Lys  
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 20 25 30

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 35 40 45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu  
 50 55 60

Asn Lys  
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<210> 103  
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 <222> (11)..(1123)

<400> 103

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              1              5              10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac      97
Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
      15              20              25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt      145
Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
      30              35              40              45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag      193
Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
              50              55              60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt      241
Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
              65              70              75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct      289
Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
      80              85              90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt      337
Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
      95              100              105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag      385
Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
      110              115              120              125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag      433
Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
              130              135              140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga      481
Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
      145              150              155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag      529
Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
      160              165              170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc      577
Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
      175              180              185

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atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625  
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu  
 190 195 200 205  
 ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673  
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly  
 210 215 220  
 tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721  
 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr  
 225 230 235  
 gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769  
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln  
 240 245 250  
 aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817  
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr  
 255 260 265  
 att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865  
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr  
 270 275 280 285  
 ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913  
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val  
 290 295 300  
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 Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro  
 305 310 315  
 tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009  
 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val  
 320 325 330  
 cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057  
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg  
 335 340 345  
 gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105  
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr  
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 Leu Asn Thr Glu Leu  
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&lt;210&gt; 104

&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 104

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His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr	20	25	30
Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
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<212> DNA
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Ala	Lys	Thr	Met	Ala	Ala	Asn	Lys	Asp	Lys	Asp	Lys	Asp	Lys	Lys	Lys			
			15					20					25					
ccc	atc	tct	cgc	tct	gct	cgt	gct	ggg	att	cag	ttt	cca	gtt	gga	cga			148
Pro	Ile	Ser	Arg	Ser	Ala	Arg	Ala	Gly	Ile	Gln	Phe	Pro	Val	Gly	Arg			
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Ile	His	Arg	Gln	Leu	Lys	Thr	Arg	Val	Ser	Ala	His	Gly	Arg	Val	Gly			
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gcc	act	gca	gcc	gtc	tac	aca	gct	tca	atc	ctg	gag	tat	ctg	aca	gca			244
Ala	Thr	Ala	Ala	Val	Tyr	Thr	Ala	Ser	Ile	Leu	Glu	Tyr	Leu	Thr	Ala			
60					65					70					75			
gag	gtt	ctt	gag	ttg	gct	ggg	aat	gcg	agc	aag	gat	ctc	aaa	gtg	aag			292
Glu	Val	Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ser	Lys	Asp	Leu	Lys	Val	Lys			
				80					85					90				
agg	ata	acg	cca	agg	cat	ctg	cag	ttg	gcg	att	aga	gga	gat	gag	gag			340
Arg	Ile	Thr	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Gly	Asp	Glu	Glu			
			95					100					105					
ctg	gac	aca	ctc	atc	aag	gga	acg	att	gct	gga	ggg	ggg	gtg	atc	cct			388
Leu	Asp	Thr	Leu	Ile	Lys	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Val	Ile	Pro			
		110					115					120						

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430  
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 35 40 45  
 Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val  
 50 55 60  
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu  
 65 70 75 80  
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg  
 85 90 95  
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile  
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tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
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Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769



Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg  
 240 245 250  
 ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag 817  
 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu  
 255 260 265  
 agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865  
 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro  
 270 275 280  
 att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913  
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 Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser  
 35 40 45  
 Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val  
 50 55 60  
 Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro  
 65 70 75 80  
 Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg  
 85 90 95  
 Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr  
 100 105 110  
 Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His  
 115 120 125  
 Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln  
 130 135 140  
 Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser  
 145 150 155 160  
 Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr  
 165 170 175

Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly  
                     180                    185                    190  
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His  
                     195                    200                    205  
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp  
                     210                    215                    220  
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn  
                     225                    230                    235                    240  
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn  
                     245                    250                    255  
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro  
                     260                    265                    270  
 Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu  
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gatacctaaa ccaaattccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga	171
Met Ala Glu Glu Ala Lys Ser Lys Gly	
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aac gca gct ttc tct tcc ggc gat tac gcc acc gca ata acc cat ttc	219
Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe	
10 15 20 25	
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Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn	
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aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca	315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser	
45 50 55	
gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat	363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr	
60 65 70	
agc cga tta ggt gct gcg ttt att gga ttg tcc aag ttt gat gaa gcg	411
Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala	
75 80 85	
gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg	459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met	
90 95 100 105	
ctt aaa tcg gga tta gct gat gct tcg aga tct agg gtt tcg tca aag	507
Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys	
110 115 120	
tcg aat cct ttt gtt gat gcg ttt caa ggg aag gag atg tgg gag aag	555
Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys	
125 130 135	
ttg acg gcg gat ccg ggg act agg gtt tat ttg gag cag gat gat ttt	603
Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe	
140 145 150	
gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg	651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu	
155 160 165	
tat atg aag gat aag aga gtt atg aag gct tta ggg gtt ttg ttg aat	699
Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn	
170 175 180 185	
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Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala	
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gat gag agg aaa gag cct gaa ccg gag atg gaa cct atg gag ttg acg	795
Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr	
205 210 215	
gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag	843

Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu  
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 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala  
 235 240 245  
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 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser  
 250 255 260 265  
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 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
 270 275  
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 280 285  
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 Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe  
 290 295 300  
 aag atg ata gca aga gct ctg act aga aaa gga tct gct cta gtg aaa 1552  
 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys  
 305 310 315  
 atg gcg aga tgc tcg aaa gac ttt gag cct gcg att gag act ttc cag 1600  
 Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln  
 320 325 330  
 aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac 1648  
 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn  
 335 340 345  
 gat gct gag aaa gtc aag aaa gag ctg gag caa cag gag tac ttt gat 1696  
 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp  
 350 355 360 365  
 cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747  
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G  
 370 375

202

207

Val Gln Val Arg  
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<211> 558

<212> PRT

<213> Arabidopsis thaliana

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35 40 45  
Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu  
50 55 60  
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65 70 75 80  
Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly  
85 90 95  
Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp  
100 105 110  
Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala  
115 120 125  
Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr  
130 135 140  
Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile  
145 150 155 160  
Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val  
165 170 175  
Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser  
180 185 190  
Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu  
195 200 205  
Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys  
210 215 220  
Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

225                      230                      235                      240  
 Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala  
                                  245                                   250                                   255  
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                                  260                                   265                                   270  
 Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp  
                                  275                                   280                                   285  
 Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile  
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 Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg  
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 Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu  
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 Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu  
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 Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile  
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 Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys  
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 Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro  
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 Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu  
                                  420                                   425                                   430  
 Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe  
                                  435                                   440                                   445  
 Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu  
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 Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys  
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 Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu  
                                  485                                   490                                   495  
 Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn  
                                  500                                   505                                   510  
 Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu  
                                  515                                   520                                   525  
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530

535

540

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 atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171  
           Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys  
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ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219  
 Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu  
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aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g 265  
 Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G  
                                   35                                  40                                  45

gtatgtatta cttaaaactc acttttgatt taaaattggc actgagagtt tccaaatagt 325  
 actttgagac cgtgggtcgtg ttaaatttgt gtgttgatga tatttattta catggatatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432  
 ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr  
                                   50                                  55                                  60

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                                   65                                  70                                  75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525  
 Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar  
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27

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Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
 10           15           20           25

cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc      147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
           30           35           40

act g gtacaccaac gccacagtta tattttttaaa cggaacatt ttgaaattaa      201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga      258
                               ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg      306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
 45           50           55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc      354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
 60           65           70           75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac      407
Tyr

aataaaaaaat aacattttct tgaaacacta acgggtcaaatt cattgatatg tctatag      464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc      512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
           80           85           90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt      560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
           95           100           105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac      608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
 110           115           120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac      656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
125           130           135           140

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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc 712  
Ile Val

aaaacaaaaa atcaccatctt actgttttaaa aaaaccttag tttaacgtgg gggtgttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821  
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn  
145 150 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta 869  
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val  
160 165 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917  
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu  
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965  
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp  
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013  
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser  
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061  
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala  
220 225 230 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat 1109  
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr  
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157  
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys  
255 260 265

cgt gct tga aaataattgc atacgtacgt tgcaatgatc atgt 1200  
Arg Ala  
270

&lt;210&gt; 116

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 116

Met Phe Ile Arg Val Ser Ala Arg Pro Ala Thr Phe Val Glu Asp Phe  
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Lys Ala Ala Trp Ser Glu Ser His Ile Arg Gln Met Glu Asp Gly Lys  
20 25 30

Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser  
35 40 45

Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile  
 50 55 60  
 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp  
 65 70 75 80  
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg  
 85 90 95  
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys  
 100 105 110  
 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp  
 115 120 125  
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr  
 130 135 140  
 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn  
 145 150 155 160  
 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp  
 165 170 175  
 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp  
 180 185 190  
 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly  
 195 200 205  
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp  
 210 215 220  
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg  
 225 230 235 240  
 Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp  
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 Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys Arg Ala  
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[illegible]



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Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile	
220 225 230	
ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct	771
Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
285 290 295	
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
300 305 310	
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga	1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
330 335 340 345	
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt	1107
Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
350 355 360	
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt	1155
Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys	
365 370 375	
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg	1203
Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
380 385 390	
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt	1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
395 400 405	
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa	1299
Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
410 415 420 425	
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa	1347
Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
430 435 440	
ggt atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

Gly Ile Asp Ile Lys Asn Ile Gln Trp Ser Gln His  
445 450

cca

1399

&lt;210&gt; 118

&lt;211&gt; 453

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 118

Met Ala Ser Lys Val Ile Ser Ala Thr Ile Arg Arg Thr Leu Thr Lys  
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Pro His Gly Thr Phe Ser Arg Cys Arg Tyr Leu Ser Thr Ala Ala Ala  
20 25 30

Ala Thr Glu Val Asn Tyr Glu Asp Glu Ser Ile Met Met Lys Gly Val  
35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro  
50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu  
65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu  
85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala  
100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn  
115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His  
130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg  
145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr  
165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp  
180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val  
195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro  
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Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val  
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224

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&lt;222&gt; (2697) .. (3076)

&lt;400&gt; 119

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        1             5             10

ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata 97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile
  15             20             25             30

ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta 145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu
              35             40             45

caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr
              50             55             60

gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr
      65             70             75

att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc 289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
      80             85             90

tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc 337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
  95             100             105             110

aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag 385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln
              115             120             125

aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc 433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe
              130             135             140

tca ccg gag ttt cgt aaa tta cga gtc ctc gaa ttg gaa tca aac ctc 481
Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu
      145             150             155

ttc acc ggt gag att cct caa agt tac ggg aga ctc act gct ctg caa 529
Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln
      160             165             170

gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt 577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe
      175             180             185             190

ttg ggt tat ctg act gag tta act cgt ctt gat ctc gct tac atc agt 625
Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser
              195             200             205

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ttt gat cct agt ccg att cca tca acc ttg ggg aac ttg tcg aat ctg Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu 210 215 220	673
act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp 225 230 235	721
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn 240 245 250	769
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val 255 260 265 270	817
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu 275 280 285	865
agt atc gga aat tta acc gaa ttg agg aat ttt gat gtc tcg cag aat Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn 290 295 300	913
aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile 305 310 315	961
tct ttc aat ctc aat gat aat ttc ttc acc gga gga tta cca gat gtc Ser Phe Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val 320 325 330	1009
gta gct ttg aat cct aat ctc gtt gaa ttc aaa atc ttc aac aac agt Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser 335 340 345 350	1057
ttc acg ggg acg tta cca agg aat ctc ggg aaa ttc tca gaa atc tct Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser 355 360 365	1105
gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr 370 375 380	1153
ttg tgc tac aga aga aaa ctt cag aag att atc acc ttc agc aat caa Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln 385 390 395	1201
tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn 400 405 410	1249
tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg 415 420 425 430	1297
ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa	1345

Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln	
435 440 445	
tta caa ggt tct att cct cct tct att tcc aaa gct cgt cat cta tct	1393
Leu Gln Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser	
450 455 460	
cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa	1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
465 470 475	
ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt	1489
Leu Cys Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser	
480 485 490	
ttc tta gga tca att ccg tct tgc atc aac aaa ttg aag aat cta gag	1537
Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu	
495 500 505 510	
aga gta gag atg cag gag aac atg ctc gac ggc gag att ccg agt tca	1585
Arg Val Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser	
515 520 525	
gtg agt tct tgc acc gag tta acc gaa tta aat ctc tcc aac aac cgt	1633
Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg	
530 535 540	
tta cga ggc ggg ata cca ccg gaa ctc ggt gat tta ccg gtt tta aac	1681
Leu Arg Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn	
545 550 555	
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Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
560 565 570	
ctg ttg agg ctc aag ctt aat caa ttc aac gtc tcc gat aac aaa ctc	1777
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575 580 585 590	
tat g gtaagattcc ttctggattt cagcaagata tttttcgacc cagtttctta g gt	1834
Tyr G ly	
aac ccg aat ctc tgt gcc cca aat ttg gat ccg att aga cct tgc cga	1882
Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
595 600 605	
tcc aaa ccg gaa acc ccg tac att ctc cca atc tca atc ctc tgc atc	1930
Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg	1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
tta ttc aag aga aaa ccg aaa ccg acc aac aaa ata acc atc ttc cag	2026
Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln	
645 650 655	

cgg gtc ggg ttc acg gag gaa gac ata tac ccg caa tta aca gaa gat	2074
Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp	
660 665 670	
aac ata att ggg tcg ggc ggg tcg ggt ttg gtt tat aga gtg aaa ctc	2122
Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu	
675 680 685	
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Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly	
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Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu	
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Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser	
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Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly	
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Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp	
785 790 795 800	
gtc aaa agc aat aat ata ttg ttg gac cat gag atg aag cca cgt gtc	2506
Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val	
805 810 815	
gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt	2554
Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly	
820 825 830	
gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att	2602
Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile	
835 840 845	
gct ccg g gttcgaattc ttagctctac aatatcaaat cgttaaaacc ctatacgcaa	2659
Ala Pro G	
850	
gcgttttagt aacattactg ttcttctgtg gatgcag aa tat ggt tat acg tca	2713
lu Tyr Gly Tyr Thr Ser	
855	

aaa gtg aat gag aag agc gat gtc tat agc ttc ggg gtg gtt tta ctc 2761  
 Lys Val Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu  
 860 865 870

gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat 2809  
 Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn  
 875 880 885

aag gac att gtt aag ttt gca atg gaa gca gct ttg tgt tac cct tct 2857  
 Lys Asp Ile Val Lys Phe Ala Met Glu Ala Ala Leu Cys Tyr Pro Ser  
 890 895 900

cca tca gca gaa gac gga gcc atg aat caa gat tca ctt gga aac tat 2905  
 Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr  
 905 910 915 920

cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga 2953  
 Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg  
 925 930 935

gag tat gaa gag ata gag aaa gtt ctt gac gtt gca ttg ctc tgt acg 3001  
 Glu Tyr Glu Glu Ile Glu Lys Val Leu Asp Val Ala Leu Leu Cys Thr  
 940 945 950

tcg tct ttt cct atc aac agg ccg acc atg agg aaa gta gta gag ttg 3049  
 Ser Ser Phe Pro Ile Asn Arg Pro Thr Met Arg Lys Val Val Glu Leu  
 955 960 965

ctt aaa gag aag aaa tca cta gag tga tattaatcct aggcctttaa 3096  
 Leu Lys Glu Lys Lys Ser Leu Glu  
 970 975

ttattaggct tctataatgt acaaaatccg actaggattg ttactcatta ttatagccat 3156  
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&lt;210&gt; 120

&lt;211&gt; 976

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 120

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Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile Leu Ser  
 20 25 30

Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu Gln Asp  
 35 40 45

Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile  
 50 55 60

Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp  
 65 70 75 80



Leu	Ser	Gly	Tyr	Asn 85	Ile	Ser	Gly	Gly	Phe 90	Pro	Tyr	Gly	Phe	Cys 95	Arg
Ile	Arg	Thr	Leu 100	Ile	Asn	Ile	Thr	Leu 105	Ser	Gln	Asn	Asn	Leu 110	Asn	Gly
Thr	Ile	Asp 115	Ser	Ala	Pro	Leu	Ser 120	Leu	Cys	Ser	Lys	Leu 125	Gln	Asn	Leu
Ile	Leu 130	Asn	Gln	Asn	Asn	Phe 135	Ser	Gly	Lys	Leu	Pro 140	Glu	Phe	Ser	Pro
Glu 145	Phe	Arg	Lys	Leu	Arg 150	Val	Leu	Glu	Leu	Glu 155	Ser	Asn	Leu	Phe	Thr 160
Gly	Glu	Ile	Pro	Gln 165	Ser	Tyr	Gly	Arg	Leu 170	Thr	Ala	Leu	Gln	Val 175	Leu
Asn	Leu	Asn	Gly 180	Asn	Pro	Leu	Ser	Gly 185	Ile	Val	Pro	Ala	Phe 190	Leu	Gly
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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 00/08187</b> <b>(43) International Publication Date:</b> 17 February 2000 (17.02.00)
<b>(21) International Application Number:</b> PCT/EP99/05652 <b>(22) International Filing Date:</b> 4 August 1999 (04.08.99) <b>(30) Priority Data:</b> 98202634.6      4 August 1998 (04.08.98)      EP <b>(71) Applicant (for all designated States except US):</b> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijnvischstraat 120, B-9052 Zwij- naarde (BE). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LEE, Jeong, Hee [KR/BE]; Spinnmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). <b>(74) Agent:</b> DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		<b>(81) Designated States:</b> AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i> <b>(88) Date of publication of the international search report:</b> 29 June 2000 (29.06.00)
<b>(54) Title:</b> GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS  <b>(57) Abstract</b> <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table I as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/EP 99/05652

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/82 C12N15/10 C12N9/12 C12N5/10 C12Q1/68  
A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>PRÄNDL, R., ET AL. : "HSF3, a new heat shock factor from Arabidopsis thaliana, derepresses the heat shock response and confers thermotolerance when overexpressed in transgenic plants"</p> <p>MOLECULAR AND GENERAL GENETICS, vol. 258, May 1998 (1998-05), pages 269-278, XP002135096</p> <p>the whole document</p> <p style="text-align: center;">--- -/--</p>	<p>2,3,7,8, 11-14, 16,18, 21, 24-26, 28-37</p>

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents :

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- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

10 April 2000

Date of mailing of the international search report

27.04.00

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Fax: (+31-70) 340-3016

Authorized officer

Holtorf, S

# INTERNATIONAL SEARCH REPORT

Int .tional Application No  
PCT/EP 99/05652

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>KUSHNIR, S., ET AL.: "characterization of Arabidopsis thaliana cDNAs that render yeasts tolerant toward the thiol-oxidizing drug diamide"</p> <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 92, November 1995 (1995-11), pages 10580-10584, XP002127804 see also last paragraph the whole document</p>	1,2
Y	<p>WO 96 39020 A (UNIV CALIFORNIA) 12 December 1996 (1996-12-12) the whole document</p>	1,2
Y	<p>QUINTERO, F.J., ET AL.: "the SAL1 gene of Arabidopsis, encoding an enzyme with 3' (2'), 5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase activities, Increases salt tolerance in yeast"</p> <p>THE PLANT CELL, vol. 8, March 1996 (1996-03), pages 529-537, XP002092755 see last paragraph the whole document</p>	1,2
Y	<p>BABIYCHUK, E., ET AL.: "Arabidopsis thaliana NADPH oxidoreductase homologs confer tolerance of yeasts towards the thiol-oxidizing drug Diamide"</p> <p>THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 44, 1995, pages 26224-26231, XP002127805 see last paragraph the whole document</p>	1,2
Y	<p>GIRAUDAT J ET AL: "ISOLATION OF THE ARABIDOPSIS AB13 GENE BY POSITIONAL CLONING"</p> <p>PLANT CELL, US, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, vol. 4, 1 October 1992 (1992-10-01), pages 1251-1261, XP002063682 ISSN: 1040-4651 the whole document</p>	1,2
Y	<p>WO 97 41152 A (UNIV NEW YORK) 6 November 1997 (1997-11-06) page 59, line 1 - line 5</p>	1,2

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/EP 99/05652

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NAMBARA, E., ET AL.: "a mutant of Arabidopsis which is defective in seed development and storage protein accumulation is a new abi3 allele" THE PLANT JOURNAL, vol. 2, no. 4, 1992, pages 435-441, XP002129247 the whole document	1,2
A	HELM, K.W. AND VIERLING, E.: "an Arabidopsis thaliana cDNA clone encoding a low molecular weight heat shock protein" NUCLEIC ACID RESEARCH, vol. 17, no. 19, 1989, page 7995 XP002129295 the whole document	1,2
A	YANG H ET AL: "Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, GB, ELSEVIER SCIENCE PUBLISHERS, BARKING, vol. 184, no. 1, 3 January 1997 (1997-01-03), pages 83-88, XP004093225 ISSN: 0378-1119 the whole document	1,2
A	MIZOGUSHI, T., ET AL.: "characterization of two cDNAs that encode MAP kinase homologues in Arabidopsis thaliana and analysis of the possible role of auxin in activating such kinase activities in cultured cells" THE PLANT JOURNAL, vol. 5, no. 1, 1994, pages 111-122, XP002129296 the whole document	1,2
P,X	LEE, J.H., ET AL.: "a highly conserved kinase is an essential component for stress tolerance in yeast and plant cells" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 96, May 1999 (1999-05), pages 5873-5877, XP002127807 the whole document	1,2

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/EP 99/05652

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1,2-4,7,8,10-14,16-37 ( inventions 1,3,37 )
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1 completely ; 2 partially

A method to identify cDNAs involved in environmental stress tolerance in plants by expressing a silique-specific cDNA library obtained from said plant in yeast cells and screening the yeast cells for enhanced environmental stress tolerance or resistance.

2. Claims: 5,6,15 completely , 2,3,4,11,12,13,14, 18-37 partially

An isolated cDNA as identified by SEQID 1 coding for a DBF2-related peptide characterized by SEQID 2; furthermore the use of the cDNA in methods to produce transgenic plants with enhanced environmental stress tolerance or resistance.

3. Claims: 10,17 completely , 2,3,4,11,12,13,14, 18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 5 coding for a c74-related peptide characterized by SEQID 6.

4. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 7 coding for a ADH2-related peptide characterized by SEQID 8.

5. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 9 coding for a catalase /catalase3-related peptide characterized by SEQID 10.

6. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 11 coding for a HSP90-related peptide characterized by SEQID 12.

7. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

by SEQID 13 coding for a peptide similar to a phosphoenolpyruvate carboxylase characterized by SEQID 14.

8. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 15 coding for a PR-protein characterized by SEQID 16.

9. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 17 coding for a protein similar to an ascorbate peroxidase characterized by SEQID 18.

10. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 19,21 coding for a protein similar to a phosphatase binding protein characterized by SEQID 20,22.

11. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 23,25 coding for a protein similar to a retinol dehydrogenase characterized by SEQID 24,26.

12. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 27,29 coding for a protein similar to a ribosomal protein characterized by SEQID 28,30.

13. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 31 coding for a protein similar to a protein transporter characterized by SEQID 32.

14. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 33 coding for a protein similar to a peptide transporter characterized by SEQID 34.

15. Claims: 2,3,4,11,12,13,14,18-37 partially

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 35 coding for an LCT1-related protein characterized by SEQID 36.

## 16. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 37 coding for an CYC1-related protein characterized by SEQID 38.

## 17. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 39 coding for an OSM1-related protein characterized by SEQID 40.

## 18. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 41 coding for an CUP1-related protein characterized by SEQID 42.

## 19. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 43 coding for an RAD7-related protein characterized by SEQID 44.

## 20. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 45 coding for an apocytochrome b-related protein characterized by SEQID 46.

## 21. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 47 coding for an LPPL1-related protein characterized by SEQID 48.

## 22. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 49 coding for a protein similar to an auxin binding protein characterized by SEQID 50.

## 23. Claims: 2,3,4,11,12,13,14,18-37 partially

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 51 coding for an CBP57-related protein characterized by SEQID 52.

## 24. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 53 coding for a calcineurin B-related protein characterized by SEQID 54.

## 25. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 55 coding for a calnexin-related protein characterized by SEQID 56.

## 26. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 57 coding for a calreticulin-related protein characterized by SEQID 58.

## 27. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 59,61 coding for a calmodulin-related protein characterized by SEQID 60,62.

## 28. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 63 coding for a DdMek1-related protein characterized by SEQID 64.

## 29. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 65 coding for an adenosine kinase-related protein characterized by SEQID 66.

## 30. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 67 coding for a human tyrosine kinase-related protein characterized by SEQID 68.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

31. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 69 coding for an ice-plant tyrosine kinase-related protein characterized by SEQID 70.

32. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 71 coding for a kinase C receptor-related protein characterized by SEQID 72.

33. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 73 coding for a HAT7-related protein characterized by SEQID 74.

34. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 75 coding for a RSEB-related protein characterized by SEQID 76.

35. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 77 coding for a phosphatase 2C-related protein characterized by SEQID 78.

36. Claims: 2,3,4,11,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 121 potentially coding for a caltractin-related protein.

37. Claims: 7,8,16 completely; 2,3,11,13,14,18-37 partially

Idem as invention 1; but limited to the cDNA as identified by SEQID 3 coding for a HSP17.6-related protein characterized by SEQID 4.

38. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 79,81 coding for a LEA-related protein characterized by SEQID 80,82.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

39. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 83 coding for a protein similar to a PR-protein characterized by SEQID 84.

40. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 85 coding for a peroxidase-related protein characterized by SEQID 86.

41. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 87 coding for a ribosomal protein characterized by SEQID 88.

42. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 89 coding for a SAS1-related protein characterized by SEQID 90.

43. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 91 coding for a AIG2-related protein characterized by SEQID 92.

44. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 93 coding for a MT1c-related protein characterized by SEQID 94.

45. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 95 coding for a IPP2-related protein characterized by SEQID 96.

46. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 97 coding for a chlorophyll a/b binding protein protein characterized by SEQID 98.



## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

47. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention ; but limited to the cDNA as identified by SEQID 99 coding for glutathione transferase characterized by SEQID 100.

48. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 101 coding for kin1-related protein characterized by SEQID 102.

49. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 103 coding for Atmpk1-related protein characterized by SEQID 104.

50. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 105 coding for H2A-related protein characterized by SEQID 106.

51. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 107 coding for a protein with unknown function as characterized by SEQID 108.

52. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 109 coding for a protein with unknown function as characterized by SEQID 110.

53. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 111 coding for a protein with unknown function as characterized by SEQID 112.

54. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 113 coding for a protein with unknown function as

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

characterized by SEQID 114.

55. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 115 coding for a protein with unknown function as characterized by SEQID 116.

56. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 117 coding for a protein with unknown function as characterized by SEQID 118.

57. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 119 coding for a protein with unknown function as characterized by SEQID 120.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 99/05652

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# A tormentor in the quest for plant p53-like proteins

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**Abstract** Over the past few years the presence of p53-like proteins in plants was frequently reported, by using the monoclonal antibody Pab240. By means of protein purification and screening a cDNA library, a Pab240 cross-reacting protein and a cDNA clone were isolated from barley. Peptide- and DNA-sequence analysis identified one and the same protein: 2-oxoglutarate dehydrogenase. Sequence analysis of 2-oxoglutarate dehydrogenase revealed that the protein contains a perfect Pab240 epitope. In barley, the 110 kDa oxoglutarate dehydrogenase was degraded during isolation to a 53 kDa Pab240 cross-reacting polypeptide, thereby mimicking curiously p53-like properties. © 2002 Federation of European Biochemical Societies. Published by Elsevier Science B.V. All rights reserved.

**Key words:** 2-Oxoglutarate dehydrogenase; p53; Pab240; Immuno recognition; Barley

## 1. Introduction

Since the first reports that a mechanism of programmed cell death (PCD) occurs in animal as well as in plant cells, research has been focussed on whether typical pathways leading to PCD are conserved among these two kingdoms. Although the majority of the key proteins involved in PCD pathways are highly conserved in animal cells, only a very limited number of counterparts were identified in plants thus far, based on sequence homology. One of the key regulatory proteins of the mammalian apoptotic machinery is tumour suppressor p53. In mammals it is known that p53 mediates G1 arrest following DNA damage in order to allow DNA repair or, in case of severe DNA damage, to induce apoptosis (recently reviewed by Bargonetti and Manfredi [1]). This dual role makes p53 the guardian of the genome integrity. In spite of the fact that several homologues of animal proto-oncogene and tumour suppressor gene-related proteins, like *c-myc*, *c-fos* and *c-jun*, as well as cell cycle regulatory proteins, like retinoblastoma, were identified in plants [2], a putative plant p53 is still not identified. However, several reports appeared in the past ten years speculating on the presence of a putative p53 in plant cells. By using the monoclonal antibody Pab240, recognising a

five amino acid stretch in the central core of the murine p53, cross-reactivity with polypeptides in the range of 53–100 kDa has been found in *Zea mays* [3,4] and *Pisum sativum* [5,6]. The presence and intensity of these cross-reactive bands were often correlated with DNA repair, especially during seed germination [3–7]. Such a correlation is quite conceivable since it has been established that aged seeds contain high levels of DNA damage, occurring during storage of seeds [8] and aged seeds do have an increased mean germination time relative to their unaged counterparts, probably due to an extension of the G1 phase to allow DNA repair [7]. So if it is a question of the presence of a plant p53 homologue, indeed one expects to find it in this stage of plant development.

In our previous experiments, cross-reactivity with 53, 73 and 110 kDa polypeptides with the Pab240 antibody were found in barley suspension cells as well as in germinating barley seeds (unpublished data). In concert with the results reported from pea and maize [3–6] the intensity of the immunostained bands was increased dramatically during the early stage of germination but also after exposure of the suspension cells to UV-B radiation. In this study these cross-reactive polypeptides were identified from protein purification as well as from isolation of cross-reacting clones from a barley cDNA expression library. Both approaches reveal that the cross-reacting polypeptides are *not* putative plant p53 homologues but 2-oxoglutarate dehydrogenase, a complex-forming enzyme involved in the Krebs cycle but containing an ideal epitope to be recognised by the Pab240 antibody.

## 2. Materials and methods

### 2.1. Plant material

Embryonic cell suspensions were from barley (*Hordeum vulgare* L. cv. Igri) immature in vivo embryo-derived callus (12 days after flowering) as described by Korthout et al. [9].

### 2.2. Protein purification

About 900 g fresh-weight embryonic suspension cells were harvested by filtration over one layer Whatman paper no. 1. The cells were homogenised in a buffer (100 ml for each 100 g cells) containing 25 mM Tris-Cl pH 7.5, 0.44 M sucrose, 10 mM MgCl<sub>2</sub>, 1 mM dithiothreitol (DTT), 0.1% (w/v) Triton X-100 and 0.1 mM phenylmethylsulfonyl fluoride (PMSF) using an Ultrathurrax (Janke and Kunkel, Staufen, Germany; three pulses at 24 000 rpm of 30 s intervals). The homogenate was filtrated over two layers of cheesecloth and subsequently centrifuged for 5 min at 600 × g to obtain the cellular debris and 20 min at 50 000 × g to obtain the cytosolic extract. Hence, Pab240 reactive protein(s) were isolated from the cytosolic extract by a three-step purification protocol. The first step consists of ammonium sulphate precipitation. All Pab240 reactive proteins precipitate 55–65% of saturated ammonium sulphate. After dialysis (o/n at 4°C against a buffer containing 25 mM Tris-Cl pH 7.5, 1 mM DTT and 0.1 mM PMSF, using Spectra/por 25 mm cellulose dialyse tubing;

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m.w. cut-off 12000–14000; Spectrum Medical Industries, Los Angeles, CA, USA) the dialysate was loaded on a 6 ml Resource-Q column connected to a FPLC-system (Amersham Biosciences, Uppsala, Sweden). Pab240 reactive proteins were eluted between 0.40 and 0.45 M NaCl in dialyse buffer. The Pab240 reactive proteins were further purified by means of preparative SDS-PAGE and fractions containing proteins with molecular masses ranging between 105 and 125 kDa were collected. These fractions were pooled, concentrated by means of ultra-filtration (Diaflow 10YM30 ultra-filtration membranes, Amicon Corporation, Beverly, MA, USA) and dialysed against a buffer containing 25 mM Tris-Cl pH 7.5 and 5 mM EDTA (o/n 4°C). Thereafter ATP was added to a final concentration of 6 mM and the proteins were digested with trypsin (20 µg/ml, 50 min, 23°C). The digest was subjected to SDS-PAGE and the 73 and 53 kDa polypeptide Pab240 cross-reacting bands excised from gel and used for sequence analysis.

### 2.3. Screening of barley expression library with Pab240

An expression cDNA library was constructed by using λZAP Express® vectors according to the manufacturer's instructions (Stratagene, La Jolla, CA, USA). Total mRNA was isolated from a mixture of heat-shocked (30 min, 42°C, 24 h recovery) and control barley embryonic suspension cells. The mRNA was converted to cDNA and packed into λZAP Express® vectors. The vectors were tested on the presence of multiple-sized inserts. The average size was about 0.5–2 kbp.

Immunological screening of the expression library with Pab240 was performed as described by Sambrook et al. [10], starting with twelve 150 mm plates containing approximately 50 000 plaque forming units each. About 50–100 positive clones per plate were obtained after the first screen. After purification and isolation of Pab240 immuno-reactive λ-clones, the pBKCMV vectors containing the inserts were excised from the λ-clones according to the manufacturer's instructions and subjected to sequence analysis.

### 2.4. Electrophoretic separation and Western blot analysis

Samples for protein analysis were separated on a 10% SDS-PAGE gel according to Laemmli [11]. The proteins were electro-transferred to a nitrocellulose membrane (Schleicher and Schuell). For Western analysis the monoclonal antibody Pab240 (sc-99, Santa Cruz Biotechnology, Santa Cruz, CA, USA) was used. Visualisation was performed with goat-anti-mouse horseradish peroxidase (HRP) conjugate (Promega, Madison, WI, USA) followed by chemoluminescent detection.

Preparative electrophoresis was performed by using a Prep-Cell (model 491, Bio-Rad Laboratories, Hercules, CA, USA) on a 75 ml 6% polyacrylamide gel. During the run (at 40 mA/h) fractions of 9 ml were collected and analysed on SDS-PAGE and Western blotting.

### 2.5. Protein sequence analysis

Polypeptides excised from gel were digested in gel with trypsin extracted from gel and separated by means of preparative high-performance liquid chromatography (HPLC). The amino acid sequence analysis of the peptides was performed by means of N-terminal protein sequence analysis by using an Applied Biosystems Model 494 Procise Protein Sequencing System, on-line connected to an RP-HPLC unit for identification of the step-wise released PTH amino acids.

Sequence analysis was performed by Eurosequence (Groningen, The Netherlands).

## 3. Results

For studying the presence of p53-like proteins in plant cells, several antibodies were used. Among them the monoclonal Pab240, an antibody originally generated in monoclonal hybridomas from a mouse immunised with a β-galactosidase/murine-p53 fusion protein [12]. By epitope mapping it was

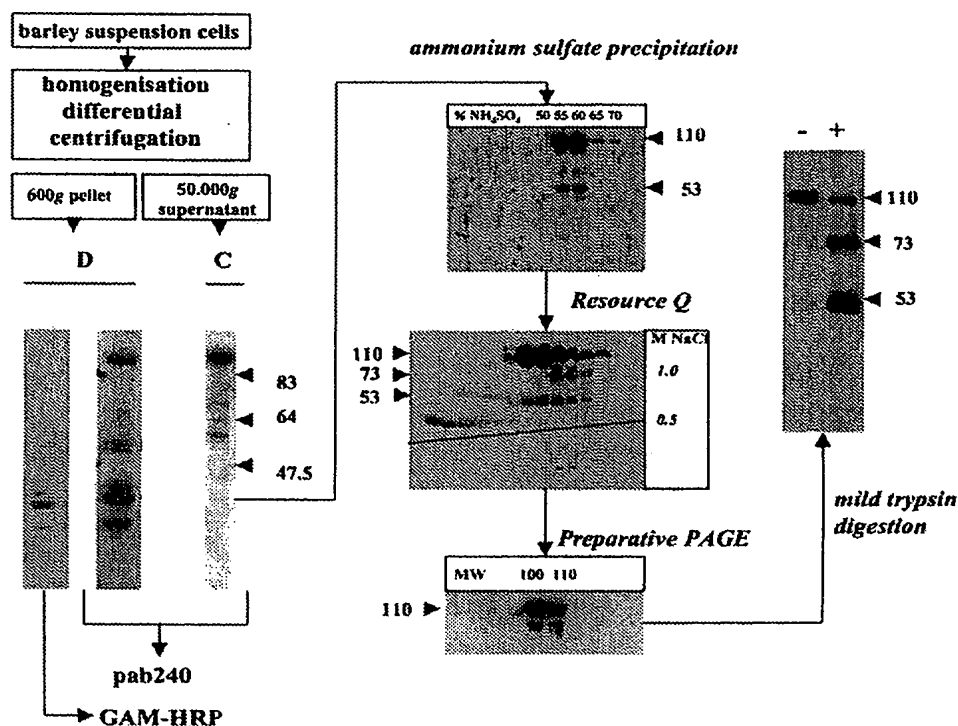


Fig. 1. Purification protocol for the isolation of the 110 kDa Pab240 cross-reactive polypeptide from barley embryonic suspension cells. After differential centrifugation, a 600×g pellet was obtained consisting of cellular debris (D; organelles and nuclei) and a 50 000×g supernatant containing the cytosolic fraction (C). The cytosolic fraction was subjected to a purification protocol comprising ammonium sulphate precipitation, anion exchange (Resource Q) and Preparative PAGE as described in Section 2. Fractions were collected and analysed on Western blots. The 110 kDa polypeptide (–) was subjected to mild trypsin digestion (+) and the 73 and 53 kDa bands were excised from gel and used for sequence analysis. The antibody utilised in all blots was Pab240. Non-specific cross-reaction caused by the secondary antibody (GAM-HRP) was found mainly to be present in the cellular debris.

At-ox:	1	MVWFRIGSSVAKLAIRRTLSQSRCSYATRTRVLPCQTRCFHISTILKSKAESAAPVPRPV	60
At-ox:	61	PLSKLTDSFLDGTSSVYLEELQRAWADPNVSDSWDNFFRNFGQASTSPGISGQTIQE	120
At-ox:	121	SMRLLLLVRAYQVNGHMKAKLDPLGLEKREIPEDLTPGLYGFTEADLDREFFLGVWRMSG	180
B-p-ox:			M+G MAG 3
At-ox:	181	FLSENRPVQTLRSILSRLEQAYCGTIGYEYMHIAADKCNWLRDKIETPTPROYNSRRM	240
B-p-ox:	4	FLSENRPVQTLRSVLARLEQAYCGTIGYEYMHIPDRKCNWLRDRIETVNPREYTYDRRO	63
At-ox:	241	VIYDRLTWSTQFENFLATKWTAKRFGLEGAEALIPCMKEMFDRSADLGVENIVIGMPHR	300
B-p-ox:	64	VMLDRLIWSQFENFLAQKWTAKRFGLEGAEALIPCMKEMFDRADLGVESIVIGMPHR	123
At-ox:	301	GRNLVGLNVVRKPLRQIFSEFSGGT+PV+E GLYTGTDGVKYHLGTSYDRPTRGKKHLH	360
B-p-ox:	124	GRNLVGLNVVRKPLRQIFSEFSGGT+KPVNEGEGLYTGTDGVKYHLGTSYDRPTRGKKHLH	183
At-ox:	361	LSLVANPSHLEAVDPVVGKTRAKQYYTKDENRTKNGILIHGDGSGFAGQGVVYETLHLS	420
B-p-ox:	184	LSLVANPSHLEAVDPVVGKTRAKQYYTNDLDRTKNLGLVLLHGDGSGFAGQGVVYETLHLS	243
At-ox:	421	ALPNYCTGGTVHVVNNQVAFITDPREGRSSQYCTDVAKALSAPIFHVNADDIEAVVHAC	480
B-p-ox:	244	ALPNYCTGGTVHVVNNQVAFITDPREGRSSQYCTDVAKALDAPIFHVNGDDLEAVVYTC	303
At-ox:	481	ELAAEWRTFHSDDVVDLVCYRRFGHNEIDEPSFTQPKMYKVRSHPSLSQIQEKLLOS	540
B-p-ox:	304	ELAAEWRTFHSDDVVDLVCYRRFGHNEIDEPSFTQPKMYKVRSHPSLSQIQEKLLOS	363
At-ox:	541	GQVTOEDIDKIQKVVSSILNEEYKSDYIPQKRDWLASHWTGFKSPEQISRIKRTGVKP	600
B-p-ox:	364	GKISKEDIDKIHKVSTILNEEFKSKDDIPNKRDLWSAYWTGLSPQXQISRIKRTGVKP	423
At-ox:	601	EILKQVKGKISTFPENFKPHRGVGRVYEQRAQMIESGEGIDWGLGEALAPATLVVEGNHV	660
B-p-ox:	424	EILKRVGEAMTTLPETFKPHRAVKKI FDLRRQMIETGEGIDWAVGEALAPATLIEGNHV	483
At-ox:	661	RLSGQDVERGTFSHRHSLVDQETGEYCPDLHLIKNDPEMFTVSNSSLSEFVGLGFEL	720
B-p-ox:	484	RLSGQDVERGTFSHRHSLVDQETGEYCPDLNLMVNEELFTVSNSSLSEFAVLGFEL	543
At-ox:	721	GYSMENPNSLVIWEAQFGDFANGAQMVFQFISSEGAKWLRQTGLVVLPHGYDQGGPEH	780
B-p-ox:	544	GYSMENPNSLVIWEAQFGDFANGAQMVFQFISSEGAKWLRQTGLVVLPHGYDQGGPEH	603
At-ox:	781	SSGRLEFLQMSDDNPYVIPMDPTLRKQIQECNQVNVVTTTPANYFHLRRQIHRDFRK	840
B-p-ox:	604	SSARMERFLQMSDDNPYVIPMDPTMRKQIQECNQVNVVTTTPANYFHLRRQIHRDFRK	663
At-ox:	841	PLIVMAPKNLLRHKQCVSNLSEFDDVKGHPGFDKQGRTRFKRLIKDQSGHSDLEEGIRRLV	900
B-p-ox:	664	PLIVMSPKNLLRHKQCVSNLSEFDDLAGHPGFDKQGRTRFKRLIKDRNDHKLDEEGIRRLV	723
At-ox:	901	LCSGKVVYELDEERKKSETKDVAICRVEQLCPFPYDLIQRELKRYPNAEIVWCQEEPMMN	960
B-p-ox:	724	LCSGKVVYELDEERKKSCDNDVAICRVEQLCPFPYDLIQRELKRYPNAEIVWCQEEPMMN	783
At-ox:	961	GGYQYIALRLCTAMKALQRGNFNDIKYVGRUPSAATATGFYQLHVKEQTDLVKKALQDP	1020
B-p-ox:	784	GAYTYINPRLLTAMRALGRGSIODIKYLGKAPSAATATCFYTVHVQEQLVKKALQDP	843
At-ox:	Arabidopsis thaliana 2-oxoglutarate dehydrogenase E1 subunit; GI: 18389253		
B-p-ox:	Barley putative 2-oxoglutarate dehydrogenase; GI: 18235680, 14525312, 19520324, 18205270, 18206048, 9419194 and 18208234		

Fig. 2. Amino acid alignment between the 2-oxoglutarate dehydrogenase E1 subunit (At-ox) and the barley homologue (B-p-ox). The barley 2-oxoglutarate dehydrogenase E1 subunit homologue is a composite constructed from overlapping sequences present in the database. Sequences obtained from four tryptic digests from the 110 kDa purified Pab240 cross-reactive polypeptide (P1–P4) were 100% identical with the under-scored sequence. Black box: Pab240 recognition site; white box: putative Pab122 recognition site.

found that this antibody recognises a five amino acid long epitope, RHSV(V/I), of human, mouse and chicken p53 [13]. In barley embryonic suspension cells, this antibody showed cross-reaction with several polypeptides ranging from 10 to 110 kDa. The cross-reaction with the small polypeptides, which were predominant in the cellular debris after centrifugation, was unspecific since cross-reaction was also observed by using only the secondary antibody GAM-HRP (Fig. 1). However, three polypeptides of 53, 73 and 110 kDa, respectively, present in the cytosolic fraction after centrifugation, specifically cross-react with the Pab240 antibody. Especially the 73 and 53 kDa polypeptides frequently appeared on blot

as doublets. The ratio between these three Pab240 cross-reactive polypeptides varied among different extracts we made. In order to find out whether these different polypeptides were related to each other and whether they represented plant p53-like proteins, a three-step purification protocol was developed as described in Section 2. The purification, as schematically depicted in Fig. 1, finally resulted in a purified 110 kDa polypeptide from the cytosolic extract which could be converted to the 73 and 53 kDa form by means of mild trypsin digestion. Both 73 and 53 kDa polypeptides were subjected to sequence analysis. First by peptide mapping it became clear that the doublets represent one and the same protein. Se-

sequence analysis resulted in the identification of four peptides (P1–P4 in Fig. 2) which were all homologues to the *Arabidopsis* 2-oxoglutarate dehydrogenase. By searching for the barley homologue in the NCBI database we were able to retrieve seven expressed sequence tags which almost fully covered the entire protein (Fig. 2). Amino acid positions 498–502 of the barley composite exposes the sequence RHSV, indeed an epitope for Pab240 [13,14]. Moreover, positions 680–684 expose a putative epitope for another p53 monoclonal antibody, Pab122.

Independently of the protein purification as described above, another approach was followed to identify the Pab240 cross-reactive protein in barley. An expression library was constructed from the total mRNA pool isolated from a mixture of heat-shocked and control barley suspension cells. First we have checked whether cross-reactivity of Pab240 occurs in *Escherichia coli* cells, the host cells of the  $\lambda$ ZAP phages. No cross-reaction could be observed. After screening of the transfected library, several Pab240 cross-reactive clones were found and subsequently isolated. One strong cross-reactive clone was selected for sequence analysis. Again this sequence showed a strong similarity with the *Arabidopsis* 2-oxoglutarate dehydrogenase (Fig. 3). These data confirm the identity of the Pab240 cross-reactive protein in barley as obtained by protein purification.

Next we wanted to find out whether the 53, 73, both often appearing as a doublet, and 110 kDa polypeptides were related to each other or different proteins carrying an epitope for Pab240. It was shown that mammalian p53s exposing the pab240 epitope are able to associate with heat-shock protein hsp70 [12]. If we heat-shocked our barley cell suspensions (10 min 42°C) at several time points prior to protein extraction we could clearly demonstrate that both the 53 and 73 kDa cross-reactive bands disappear in favour of the 110 kDa band (Fig. 4). Moreover, if the heat-shocked sample containing the 110 kDa protein (or the 110 kDa protein isolated by preparative PAGE during the purification protocol) was treated with a low concentration of trypsin, the intensity of the 110 kDa band diminished and the 73 and 53 kDa bands appeared again on Western blot. The concentration of trypsin used in

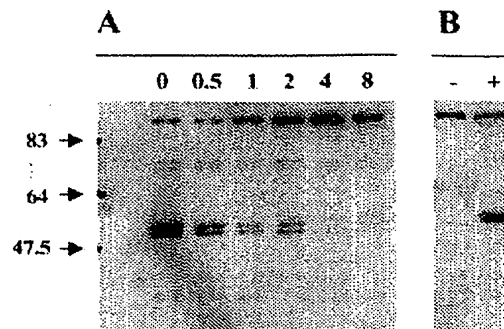


Fig. 4. A: Behaviour of the Pab240 cross-reactive polypeptides in cytosolic extracts of barley embryonic suspension cells after heat shock (10 min, 42°C). Cytosolic extracts were made prior to heat shock (0) and after 0.5, 1, 2, 4 and 8 h recovery at 28°C. B: Trypsin treatment of a cytosolic extract obtained from heat-shocked cells after 4 h recovery; (–) before trypsin treatment, (+) after 50 min incubation with 20  $\mu$ g/ml trypsin at 23°C. Both Western blots were probed with the Pab240 antibody.

these experiments was extremely critical since a small increase resulted in complete disappearance from the blot. These data strongly indicate that the 53 and 73 kDa polypeptides were degradation products of the 110 kDa polypeptide due to proteolytic activity during isolation. We suggest that binding of heat-shock proteins to the 110 kDa polypeptide in reaction to heat shock (Fig. 4A) may prevent this degradation. The fact that tryptic digests of the 53/73 kDa polypeptides, obtained during sequence analysis, display a high degree of homology with the 105 kDa 2-oxoglutarate dehydrogenase strongly supports this hypothesis.

#### 4. Discussion

In this study we have demonstrated that the cross-reactivity with the p53-specific Pab240 antibody in barley was not caused by a putative plant p53 homologue but by 2-oxoglutarate dehydrogenase, a 105 kDa subunit from a multi-enzyme assembly that occupies a central role in cellular metabolism within the tricarboxylic acid cycle. The presence of this protein combined with its biochemical features during experimental conditions causes a big obstacle for identifying p53-like proteins in plants by using Western blot techniques only. It mimics the features of the mammal p53 in several ways:

First, there is a clear recognition of the plant 2-oxoglutarate dehydrogenase by one of the best studied and frequently utilised antibodies in mammalian p53 research activities, the monoclonal Pab240. Obviously, this antibody may not be specific enough, since only a small motif of five amino acid residues, RHSV(V/I), also present at positions 498–502 of the barley 2-oxoglutarate dehydrogenase composite, allows recognition by the antibody [13,14]. It was already demonstrated that proteins containing this motif, like TFIIIA from *Xenopus laevis*, cross-react with the Pab240 [13]. Referring to Stephen et al. [14], a second interesting motif may be present on the barley 2-oxoglutarate dehydrogenase composite, KSSL, located at positions 681–685, which mimics an epitope for the p53 monoclonal Pab122 [14]. Interestingly, in pea root tips a 94 kDa protein was recognised by both Pab240 and Pab122 antibodies [5]. However, due to limited information on the Pab122 epitope, the lack of sequence information of the pea oxoglutarate dehydrogenase homologue and the fact that dif-

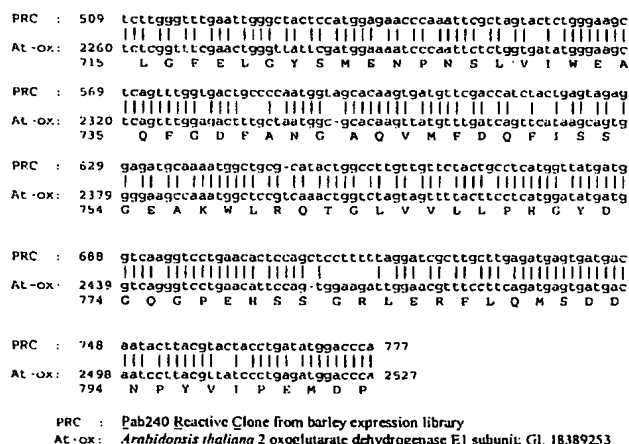


Fig. 3. Nucleotide sequence alignment between a clone isolated from the barley expression library, cross-reacting with the Pab240 antibody (PRC), and the 2-oxoglutarate dehydrogenase E1 subunit from *Arabidopsis thaliana* (At-ox). 81% identity was obtained.

ferent experimental procedures were used as compared to our study, it is not possible to predict whether cross-reactivity in pea is also caused by oxoglutarate dehydrogenase.

Second, we observed a dramatic increase in intensity of the Pab240 cross-reactive bands during the early stage of germination. In this period the machinery of DNA repair, to recover DNA integrity induced during seed maturation and storage [7,8], is fully operable. In mammalian cells p53 induces G1 arrest to allow DNA repair, so indeed one expects to find an increase of the putative plant p53 during early germination. On the other hand, during early germination also the plant cellular metabolism is fully switched on, e.g. enzymatic activity in the tricarboxylic acid cycle. Consequently, it remains unclear whether the observed increase of the Pab240 cross-reactive bands during the early stage of germination is a result of an increase of p53-related proteins involved in DNA repair or just an increase of the metabolic enzyme oxoglutarate dehydrogenase.

Third, the molecular weight of the Pab240 cross-reactive proteins in plant extracts under denaturing conditions is similar to that of mammalian p53. However, next to a 53 kDa band, a 73 and 110 kDa band were also recognised in barley extracts by the Pab240 antibody. Interestingly, the ratio of the intensity of those 53, 73 and 110 kDa bands varied within the several extracts we made. Cross-reactivity in the region of 70 and 100 kDa by the Pab240 antibody was already reported to occur in maize [3] and pea [5,6]. In this report we showed that in our experimental system, the cytosolic extract of barley suspension cells, the 53, 73 and 110 kDa bands are related to each other. Artificial proteolytic cleavage of the purified 110 kDa band by controlled trypsin digestion revealed that the 110 kDa band could be easily converted to the 73 and 53 kDa form. Moreover, with heat-shock treatment of the barley suspension cells we showed that the intensity of the 53/73 kDa bands isolated during extraction decreased dramatically in favour of the 110 kDa band. Furthermore, it was shown by Gannon et al. [12] that proteins exposing the Pab240 epitope RHSV(V/I) were able to bind heat-shock protein hsp70. These chaperones are highly conserved proteins among the animal and plant kingdom. Assuming that 2-oxoglutarate dehydrogenase exposes its RHSVI motif, the hsp70, probably present in a chaperone complex, may associate and consequently stabilise the protein, thereby preventing proteolytic cleavage during isolation, especially after heat shock. It may be interesting to note that during purification of the 110 kDa polypeptide the heat-shock protein hsp82, a member of the hsp90 family, was co-purified (data not shown). It is known that chaperone complexes may contain both hsp90 and hsp70 proteins and that these complexes are evolutionarily conserved between the animal and plant kingdom [15]. Taken together, there are strong indications that the 53, 73 and 110 kDa polypeptides represent one and the same protein, the 105 kDa 2-oxoglutarate dehydrogenase.

The fact that the Pab240 cross-reactive protein(s), obtained by protein purification as well as by screening of an expression library, was identified as 2-oxoglutarate dehydrogenase, does not exclude the possibility that more Pab240 cross-reacting proteins or even p53-related proteins exist in plant cells. For example, 2-oxoglutarate dehydrogenase is a metabolic protein present in a complex in the mitochondria, but in pea cross-

reactivity with the Pab240 was also observed in nuclei by means of immuno-localisation studies [5]. However, extreme caution must be taken by interpretation of data only obtained by immunological experiments. In our opinion, the putative plant p53, if it exists, will be a functional homologue rather than a structural one. Searching for sequence homology in plant nucleotide databases failed thus far and moreover, even among animals the p53 protein is not highly conserved. Only recently the p53 homologues of *Drosophila melanogaster* [16–18] and *Caenorhabditis elegans* [19] were identified. From these studies it became clear that only a set of five domains of the p53 were conserved. The p53 homologue of *C. elegans* could not be retrieved from public databases using standard searches and only with additional algorithms the conserved domains and therefore the p53 homologue could be identified [19]. Still, even by using these conserved domains and the additional algorithms for searching in plant databases, a plant p53 homologue could not be found. Focussing on p53's interacting partners, like the highly conserved proteins involved in cell-cycle regulation or inhibitory proteins might be a fruitful strategy for identifying the plant p53 homologue.

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